

12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045

QY 301 ACCCTGCAATTGTGCGCTTGAAGAGCTGCTGTGCTTTTGAGGCTCTGAGGAGCA 360
DB 396 ACCCTGCAATTGTGCGCTTGAAGAGCTGCTGTGCTTTTGAGGCTCTGAGGAGCA 455
QY 361 CTCATGCGCAGCTGCGAGACTCTCACTTCACTTCTGTATGAGTCACTGATGAT 420
DB 456 CTCATGCGCAGCTGCGAGACTCTCACTTCTGTATGAGTCACTGATGATGAT 515
QY 421 GAGCTGTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 480
DB 516 GAGCTGTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 575
QY 481 CAGGAGAGGCGCTTTGCGCAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 540
DB 576 CAGGAGAGGCGCTTTGCGCAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 635
QY 541 CCGGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 600
DB 636 CCGGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 695
QY 601 ACTGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 660
DB 696 ACTGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 755
QY 661 CCGCAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 720
DB 756 CCGCAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 815
QY 721 AAGCAGGAG 780
DB 816 AAGCAGGAG 875
QY 781 CTGAG 840
DB 876 CTGAG 935
QY 841 GACATCTCATCAACCGGAGAGTCAACGAGAGAGTCAACGAGAGAGTCAACGAG 900
DB 936 GACATCTCATCAACCGGAGAGTCAACGAGAGAGTCAACGAGAGAGTCAACGAG 995
QY 901 GGGGTCTTCAAGTCTTCTGCGCTTCAAGAGTGTGAGAGTGTGAGAGTGTGAG 960
DB 996 GGGGTCTTCAAGTCTTCTGCGCTTCAAGAGTGTGAGAGTGTGAGAGTGTGAG 1055
QY 961 AAGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1020
DB 1056 AAGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1115
QY 1021 ATCTGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 1080
DB 1116 ATCTGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 1175
QY 1081 TGGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 1116
DB 1176 TGGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 1211

RESULT 2
US-09-570-593-4

/ Sequence 4, Application US/09570593
/ Patent No. 6566063
/ GENERAL INFORMATION:
/ APPLICANT: Kaufmann, Joerg
/ APPLICANT: Xun, Hong
/ APPLICANT: Hartwe, Greg
/ TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
/ FILE REFERENCE: 2300-1556
/ CURRENT APPLICATION NUMBER: US/09/570, 593
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: 60/134, 112
/ PRIOR FILING DATE: 1999-05-14

/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 1907
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (96)...(1211)
/ OTHER INFORMATION: Human epithelial-restricted with serine box (ESB)
/ OTHER INFORMATION: protein.
US-09-570-593-4

Query Match 100.0%; Score 1116; DB 4; Length 1907;
Best Local Similarity 100.0%; Pred. No. 7.6e-291;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTGCACCTGTGAGATTTAGCAATTTTATGCACTTATGATGAGTGAAGC 60
DB 96 ATGAGTGCACCTGTGAGATTTAGCAATTTTATGCACTTATGATGAGTGAAGC 155
QY 61 TCGAGAGACTCCACCTGAGCTCTGTTCCTGCTGACCTTTGGGCGATGACTTG 120
DB 156 TCGAGAGACTCCACCTGAGCTCTGTTCCTGCTGACCTTTGGGCGATGACTTG 215
QY 121 GTAATGACCTTGAGCAACCCCGAGATGTATGAGAGTGAAGAGAGAGAGAG 180
DB 216 GTAATGACCTTGAGCAACCCCGAGATGTATGAGAGTGAAGAGAGAGAGAG 275
QY 181 GGGGAAACAGCCCAAGTCTGTGTCGAAGAGAGAGTGTGAGTGAAGTGAAG 240
DB 276 GGGGAAACAGCCCAAGTCTGTGTCGAAGAGAGAGTGTGAGTGAAGTGAAG 335
QY 241 GAGAGAAAG 300
DB 336 GAGAGAAAG 395
QY 301 ACCCTGCAATTGTGCGCTTGAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 360
DB 396 ACCCTGCAATTGTGCGCTTGAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 455
QY 361 CTCATGCGCAGCTGCGAGACTCTCACTTCACTTCTGTATGAGTCACTGATGAT 420
DB 456 CTCATGCGCAGCTGCGAGACTCTCACTTCACTTCTGTATGAGTCACTGATGAT 515
QY 421 GAGCTGTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 480
DB 516 GAGCTGTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 575
QY 481 CAGGAGAGGCGCTTTGCGCAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 540
DB 576 CAGGAGAGGCGCTTTGCGCAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 635
QY 541 CCGGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 600
DB 636 CCGGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 695
QY 601 ACTGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 660
DB 696 ACTGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 755
QY 661 CCGCAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 720
DB 756 CCGCAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 815
QY 721 AAGCAGGAG 780
DB 816 AAGCAGGAG 875
QY 781 CTGAG 840
DB 876 CTGAG 935

QY 841 GACATCTCATCCACCGGAGCTCAACGAGGGCTCATGAGTGGAGATCGGCATGAA 900
DB 936 GACATCTCATCCACCGGAGCTCAACGAGGGCTCATGAGTGGAGATCGGCATGAA 995
QY 901 GGGCTCTTCAAGTTCTTCCGCTCCGAGGCTGTGSCCCCACTATGGGCGCAAAAGAAAG 960
DB 996 GGGCTCTTCAAGTTCTTCCGCTCCGAGGCTGTGSCCCCACTATGGGCGCAAAAGAAAG 1055
QY 961 AACAGCAATGATCTTACGAGAGCTGAGCGGGCCATGAGTGTACTTCAAAACGGGAG 1020
DB 1056 AACAGCAATGATCTTACGAGAGCTGAGCGGGCCATGAGTGTACTTCAAAACGGGAG 1115
QY 1021 ATCTCTGAACGAGTGTGATGCGCGGAGCTGTCTCAACAGTTTGGCAAAACTCAAGCGG 1080
DB 1116 ATCTCTGAACGAGTGTGATGCGCGGAGCTGTCTCAACAGTTTGGCAAAACTCAAGCGG 1175
QY 1081 TGGAGAGAGAGAGGTTCTTCCAGAGTCCGAACTGA 1116
DB 1176 TGGAGAGAGAGAGGTTCTTCCAGAGTCCGAACTGA 1211

RESULT 3

US-08-746-789A-1
; Sequence 1, Application US/08746789A
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismail Kola, Martin J. Tyms, Christine Debouck
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELP3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,789A
; FILING DATE: No. 5789200ember 15, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG 50024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5219
; TELEFAX: 610 270 4026
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
; US-08-746-789A-1

Query Match 99.4%; Score 1109.6; DB 1; Length 1920;
Best Local Similarity 99.6%; Pred. No. 4e-289;
Matches 1112; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGCTGCAACCTGTGATTTAGCAACATTTTATGCACTACTTCACTGCGATGACG 60
DB 115 ATGGCTGCAACCTGTGATTTAGCAACATTTTATGCACTACTTCACTGCGATGACG 174
QY 61 TCGAGAGATCCACCCCTGCTGTTCCTCCCTGCTGCAACTTTTGGGGCGATGACTTG 120

DB 175 TCGAGAGATCCACCCCTGCTGTTCCTCCCTGCTGCAACTTTTGGGGCGATGACTTG 234
QY 121 GATCTGACCTTGAAGCAACCCCAAGATGTATTTGAGAGGTACAGAAAGCCAGCTGTG 180
DB 235 GATCTGACCTTGAAGCAACCCCAAGATGTATTTGAGAGGTACAGAAAGCCAGCTGTG 294
QY 181 GGGGAACAGCCCAAGTTCTGTGCAAGAGCAAGGTTCTGAGCTGATGACTTACCAAGTG 240
DB 295 GGGGAACAGCCCAAGTTCTGTGCAAGAGCAAGGTTCTGAGCTGATGACTTACCAAGTG 354
QY 241 GAGAAAGCAAGTACGACGCAAGCCGCAATTGACTTCTCAAGTGTACATGATGAGCGCC 300
DB 355 GAGAAAGCAAGTACGACGCAAGCCGCAATTGACTTCTCAAGTGTACATGATGAGCGCC 414
QY 301 ACCCTTGCATTTGTGCTTGAAGAGCTGCGCTGTGTCTTTGGGCTCTTGGGGGACCA 360
DB 415 ACCCTTGCATTTGTGCTTGAAGAGCTGCGCTGTGTCTTTGGGCTCTTGGGGGACCA 474
QY 361 CTCATGCCCAGCTGAGACCTCACTTCAGCTCTTGTATGAGTCACTTGAATCATTT 420
DB 475 CTCATGCCCAGCTGAGACCTCACTTCAGCTCTTGTATGAGTCACTTGAATCATTT 534
QY 421 GAGCTGCTGAGAGAGATGAGTGGCTTTCAGAGAGCCCTAGACCAGGCTTTGAC 480
DB 535 GAGCTGCTGAGAGAGATGAGTGGCTTTCAGAGAGCCCTAGACCAGGCTTTGAC 594
QY 481 CAGGAGACCCCTTTGGCCCAAGAGCTGTGAGACAGCTGTACAGACCCGCTTACAC 540
DB 595 CAGGAGACCCCTTTGGCCCAAGAGCTGTGAGACAGCTGTACAGACCCGCTTACAC 654
QY 541 CCGGAGAGCTGTGAG 600
DB 655 CCGGAGAGCTGTGAG 714
QY 601 ACTGATGCTTCTGAGAGCTCCCACTTCCTGAGACTCCGATGAGAGAGAGAGAGAGAG 660
DB 715 ACTGATGCTTCTGAGAGCTCCCACTTCCTGAGACTCCGATGAGAGAGAGAGAGAGAG 774
QY 661 CCGATGATGAG 720
DB 775 CCGATGATGAG 834
QY 721 AAGCAAG 780
DB 835 AAGCAAG 894
QY 781 CTCGAG 840
DB 895 CTCGAG 954
QY 841 GACATCTCATCCACCGGAGCTCAACGAGGCTCATGAGTGGAGAAATGGCATGAA 900
DB 955 GACATCTCATCCACCGGAGCTCAACGAGGCTCATGAGTGGAGAAATGGCATGAA 1014
QY 901 GGGCTTCAAGTTCTTCCGCTCCGAGGCTGTGSCCCCACTATGGGCGCAAAAGAAAG 960
DB 1015 GGGCTTCAAGTTCTTCCGCTCCGAGGCTGTGSCCCCACTATGGGCGCAAAAGAAAG 1074
QY 961 AACAGCAATGATCTTACGAGAGCTGAGCGGGCCATGAGTGTACTTCAAAACGGGAG 1020
DB 1075 AACAGCAATGATCTTACGAGAGCTGAGCGGGCCATGAGTGTACTTCAAAACGGGAG 1134
QY 1021 ATCTCTGAACGAGTGTGATGCGCGGAGCTGTCTCAACAGTTTGGCAAAACTCAAGCGG 1080
DB 1135 ATCTCTGAACGAGTGTGATGCGCGGAGCTGTCTCAACAGTTTGGCAAAACTCAAGCGG 1194
QY 1081 TGGAGAGAGAGAGGTTCTTCCAGAGTCCGAACTGA 1116
DB 1195 TGGAGAGAGAGAGGTTCTTCCAGAGTCCGAACTGA 1230

RESULT 4

Db 122 TGGCAAGCTCTTCCCGCAGCGATGTTTCTGTGACTGCAAGAGGGGGATCCAGACGG 181
QY 729 GAAGCGGAAACGAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 788
Db 182 GAAGCGGAAACGAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 241
QY 789 CAAGAAAGCAAGCAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 848
Db 242 CAAGAAAGCAAGCAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 301
QY 849 CATCCACCCGAGACTCAACAGAGGCTCATGAAAGTGGAGAAATCGGATGAAGCGCTT 908
Db 302 CATCCACCCGAGACTCAACAGAGGCTCATGAAAGTGGAGAAATCGGATGAAGCGCTT 361
QY 909 CAAGTTCCTGCGCTCCGAGGCTGTGGCCCAACTATGAGGGCCAAAGAAAAGAACAGCAA 968
Db 362 CAAGTTCCTGCGCTCCGAGGCTGTGGCCCAACTATGAGGGCCAAAGAAAAGAACAGCAA 421
QY 969 CATGACCTACGAGAACTGAGCGCGCCCATGAGGTACTACTACAAACGGAGATCTTGA 1028
Db 422 CATGACCTACGAGAACTGAGCGCGCCCATGAGGTACTACTACTACAAACGGAGATCTTGA 481
QY 1029 ACGGATGATGGCGCGGACT 1049
Db 482 ACGGATGATGGCGCGGACT 502

RESULT 9

US-09-834-759-282
Sequence 282, Application US/09834759
Patent No. 6680197
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-09-834-759-282

Query Match 44.7%; Score 499.4; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 5.3e-125;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 549 CTGTGGCGCAGAGCGCCCTTCCCTGAGCTGTGACGTCTCCACCGCAGGAGCTGGTGC 608
Db 2 CTGTGGCGCAGAGCGCCCTTCCCTGAGCTGTGACGTCTCCACCGCAGGAGCTGGTGC 61
QY 609 TTCTCGAGCTCCCACTCTCTCAAGCTCGGTGGAAGTGAAGTGAAGTGAAGTGAAGTGA 668
Db 62 TTCTCGAGCTCCCACTCTCTCAAGCTCGGTGGAAGTGAAGTGAAGTGAAGTGAAGTGA 121
QY 669 TGGCAAGCTCTTCCCGCAGAGTGTGTTTCTGACTGCAAGAGGGGATCCCAAGCAGCG 728
Db 122 TGGCAAGCTCTTCCCGCAGAGTGTGTTTCTGACTGCAAGAGGGGATCCCAAGCAGCG 181
QY 729 GAAGCGGAAACGAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 788
Db 182 GAAGCGGAAACGAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 241
QY 789 CAAGAAAGCAAGCAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 848

Db 242 CAAGAAAGCAAGCAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 301
QY 849 CATCCACCCGAGACTCAACAGAGGCTCATGAAAGTGGAGAAATCGGATGAAGCGCTT 908
Db 302 CATCCACCCGAGACTCAACAGAGGCTCATGAAAGTGGAGAAATCGGATGAAGCGCTT 361
QY 909 CAAGTTCCTGCGCTCCGAGGCTGTGGCCCAACTATGAGGGCCAAAGAAAAGAACAGCAA 968
Db 362 CAAGTTCCTGCGCTCCGAGGCTGTGGCCCAACTATGAGGGCCAAAGAAAAGAACAGCAA 421
QY 969 CATGACCTACGAGAACTGAGCGCGCCCATGAGGTACTACTACAAACGGAGATCTTGA 1028
Db 422 CATGACCTACGAGAACTGAGCGCGCCCATGAGGTACTACTACTACAAACGGAGATCTTGA 481
QY 1029 ACGGATGATGGCGCGGACT 1049
Db 482 ACGGATGATGGCGCGGACT 502

RESULT 10

US-09-590-751A-282
Sequence 282, Application US/09590751A
Patent No. 6756477
GENERAL INFORMATION:
APPLICANT: Yugu, Jiang
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C6
CURRENT APPLICATION NUMBER: US/09/590,751A
NUMBER OF SEQ ID NOS: 479
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-09-590-751A-282

Query Match 44.7%; Score 499.4; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 5.3e-125;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 549 CTGTGGCGCAGAGCGCCCTTCCCTGAGCTGTGACGTCTCCACCGCAGGAGCTGGTGC 608
Db 2 CTGTGGCGCAGAGCGCCCTTCCCTGAGCTGTGACGTCTCCACCGCAGGAGCTGGTGC 61
QY 609 TTCTCGAGCTCCCACTCTCTCAAGCTCGGTGGAAGTGAAGTGAAGTGAAGTGAAGTGA 668
Db 62 TTCTCGAGCTCCCACTCTCTCAAGCTCGGTGGAAGTGAAGTGAAGTGAAGTGAAGTGA 121
QY 669 TGGCAAGCTCTTCCCGCAGAGTGTGTTTCTGACTGCAAGAGGGGATCCCAAGCAGCG 728
Db 122 TGGCAAGCTCTTCCCGCAGAGTGTGTTTCTGACTGCAAGAGGGGATCCCAAGCAGCG 181
QY 729 GAAGCGGAAACGAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 788
Db 182 GAAGCGGAAACGAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 241
QY 789 CAAGAAAGCAAGCAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 848
Db 242 CAAGAAAGCAAGCAGCGCGCCCGGAAAGCTGAGCAAGAGTACTGTCTCGAGGG 301
QY 849 CATCCACCCGAGACTCAACAGAGGCTCATGAAAGTGGAGAAATCGGATGAAGCGCTT 908
Db 302 CATCCACCCGAGACTCAACAGAGGCTCATGAAAGTGGAGAAATCGGATGAAGCGCTT 361
QY 909 CAAGTTCCTGCGCTCCGAGGCTGTGGCCCAACTATGAGGGCCAAAGAAAAGAACAGCAA 968

Db 362 CAACTTCCTGCGCTCCGAGGCTGTGGCCCACTATGAGGCGCAAAAGAAAGAACAGCA 421
Qy 969 CATGACCTAGAGAGAGCTGAGCGGCGCCATGAGTACTACTAAGAAACGGAGATCTCTGA 1028
Db 422 CATGACCTAGAGAGAGCTGAGCGGCGCCATGAGTACTACTAAGAAAGGAGATCTCTGA 481
Qy 1029 ACGGCTGATGCGCGCGACT 1049
Db 482 ACGGCTGATGCGCGCGACT 502

RESULT 11

US-09-020-956-44/c
; Sequence 44, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 852 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-020-956-44

Query Match 15.6%; Score 173.8; DB 3; Length 852;
Best Local Similarity 69.7%; Pred. No. 3.3e-37;
Matches 225; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 758 TGAGCAAGAGTACTGGAAGTGTCTCGAGGGCAAGAGCAAGCAAGCGGCCCAAGAGCA 817
Db 450 TGAAAAAGAGCAAGACCCCTCGCAAGTGCACACCAAAAAAGCAACACCGAGAGGGA 391
Qy 818 CCACCTGTGGAGTTCATCCGGACATCTCTATCCACCCGGAGCTCAACGAGGGCTCA 877
Db 390 CTCACCTTATGGGAATTCATCCGGACATCTCTTGAACCCAGACAAAGACCCAGATTAA 331
Qy 878 TGAAGTGGAGATTCGGCATGAGAGGCTTCAAGTTCCTGCGCTCCGAGGCTGTGGCCC 937
Db 330 TAAATGGAGAACCGATCTGAGGGCGTCTTCAGGTTCTTGAATCAAGAGCGAGTGGCTC 271
Qy 938 AACTATGGGCGCAAAAGAAAGAAAGCAAGCAATGACCTTACGAGAAAGCTGAGCGGGCCA 997
Db 270 AGCTATGGGCTAAAGAAAGAAAGCAAGCAAGCATGACCTTATGAAAGCTCAGCGGAGCTA 211

Qy 998 TGAGTACTACTACAAACGGAGATCTGGAACGGGTGATGCGCGGACTCGTCTACA 1057
Db 210 TGAGATTTACTACAAAGAAAGAAATTTCTGAGCGTGTGATGAGCAAGACTGTATATA 151
Qy 1058 AGTTGGCAAAATCTCAAGCGGCTGGAGAGAGAGA 1094
Db 150 AATTTGGAGAAATGCGCGAGATGGAGAGAAATGA 114

RESULT 12

US-09-030-607-44/c
; Sequence 44, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 852 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-030-607-44

Query Match 15.6%; Score 173.8; DB 3; Length 852;
Best Local Similarity 69.7%; Pred. No. 3.3e-37;
Matches 225; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

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; NAME/KEY: misc feature
; LOCATION: (1)... (852)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-44

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Job time : 98.279 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: November 15, 2004, 21:57:02 ; Search time 624.355 Seconds
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1712	86.2	1907	14	US-10-097-340-74	Sequence 74, Appl
2	1712	86.2	1907	15	US-10-291-808-27	Sequence 27, Appl
3	1712	86.2	1915	9	US-09-964-824A-101	Sequence 101, Appl
4	1712	86.2	1915	9	US-09-964-824A-553	Sequence 553, Appl
5	1712	86.2	1915	9	US-09-880-107-3430	Sequence 3430, Appl
6	1712	86.2	1915	9	US-09-967-168A-192	Sequence 192, Appl
7	1712	86.2	1917	13	US-09-922-217-1105	Sequence 1105, Ap
8	1712	86.2	1917	13	US-10-025-380-1105	Sequence 1105, Ap
9	1712	86.2	1956	16	US-10-264-049-756	Sequence 756, App
10	1458.5	73.5	2269	15	US-09-925-301-207	Sequence 207, App
11	1458.5	73.5	2269	15	US-10-131-410-64	Sequence 64, Appl
12	928.5	46.8	626	9	US-09-922-217-853	Sequence 853, App
13	928.5	46.8	626	9	US-09-933-263-853	Sequence 853, App
14	928.5	46.8	626	13	US-10-025-380-853	Sequence 853, App
15	833.5	42.0	563	9	US-09-922-217-944	Sequence 944, App
16	833.5	42.0	563	9	US-09-933-263-944	Sequence 944, App
17	833.5	42.0	563	13	US-10-025-380-944	Sequence 944, App
18	803	40.5	502	9	US-09-604-287A-282	Sequence 282, App
19	803	40.5	502	9	US-09-834-359-282	Sequence 282, App
20	803	40.5	502	9	US-09-939-338-282	Sequence 282, App
21	803	40.5	502	10	US-09-551-621-282	Sequence 282, App
22	803	40.5	502	13	US-10-007-805-282	Sequence 282, App
23	803	40.5	502	14	US-10-076-622-282	Sequence 282, App
24	803	40.5	502	15	US-10-124-805-282	Sequence 282, App
25	765	38.5	489	9	US-09-998-598-2280	Sequence 2290, Ap
26	590.5	29.7	1426	9	US-09-925-297-309	Sequence 309, App
27	590.5	29.7	1426	15	US-10-106-698-935	Sequence 935, App
28	585	29.5	1429	9	US-09-764-864-320	Sequence 320, App
29	585	28.0	437	9	US-09-998-598-2216	Sequence 2216, Ap
30	543	27.4	852	9	US-09-759-143-44	Sequence 44, Appl
31	543	27.4	852	9	US-09-780-669-44	Sequence 44, Appl
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42	543	27.4	852	17	US-10-688-838-44	Sequence 44, Appl
43	527.5	26.6	335	9	US-09-867-701-4818	Sequence 4818, Ap
44	483.5	24.4	1435	15	US-10-017-161-1853	Sequence 1953, Ap
45	483.5	24.4	1435	15	US-10-292-798-1601	Sequence 1601, Ap

ALIGNMENTS

RESULT 1
US-10-097-340-74
; Sequence 74, Application US/10097340
; Publication No. US20030087250A1

GENERAL INFORMATION:

APPLICANT: JOHN MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi RAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel R. MEYERS
APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHWANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT

```

; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-097-340-74

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Alignment Scores:

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Score: 1712.00           Matches: 323
Percent Similarity: 92.74%      Conservative: 22
Best Local Similarity: 86.83%    Mismatches: 25
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US-08-978-217-16 (1-371) x US-10-097-340-74 (1-1907)

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QY 180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAsnValSerThrAla 199
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RESULT 2

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; Sequence 27, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McCelland, Michael
; APPLICANT: Welsh, John
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-291-808-27

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Alignment Scores:
Pred. No.: 2,54e-195      Length: 1907
Score: 1712.00           Matches: 323
Percent Similarity: 92.74%      Conservative: 22

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Best Local Similarity: 86.83% Mismatches: 25
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 Gaps: 2
 US-08-978-217-16 (1-371) x US-10-291-808-27 (1-1907)

Qy 1 MetAlaIaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
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RESULT 3
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 ; Patent No. US20020102531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horrigan, Stephen
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
 ; TITLE OF INVENTION: Sets
 ; FILE REFERENCE: 689290-73
 ; CURRENT APPLICATION NUMBER: US/09/964,824A
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US/60/236,033
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236,032
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236,028
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 583
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 ; TYPE: DNA
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 ; US-09-964-824A-101

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 Percent Similarity: 92.74% Conservative: 22
 Best Local Similarity: 86.83% Mismatches: 25
 Query Match: 86.25% Indels: 2
 Gaps: 2

US-08-978-217-16 (1-371) x US-09-964-824A-101 (1-1915)

Qy 1 MetAlaIaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
 Db 120 ATGGCTCAACCTGTGAGATTAGCAACATTTTTCAGCACTTCACTGCGATGTACAGC 179

Qy 21 SerGluAspProThrLeuAlaProAlaProPro--ThrThrPheGlyThrGluAspLeu 39
 Db 180 TCGGAGGACTCCACCTCGGCTCTGTCTCCCTCTGCTGCCACTTGTGGGCCCATGACTTG 239

Qy 40 ValLeuThrLeuAsnAngInglMetThrLeuGluGlyProGluValAspTyrThr 59
 Db 456 CTCATGCCAGCTGCGACAGACTCACTTCAGCTCTTCTGATGAGCTCAAGTGTGATATT 515

Qy 60 SerGluArgProGlnPheTyrSerLeuThrGlnValLeuGluTyrPheSerTyrGlnVal 79
 Db 276 GGGGAAACAGCCCGACTTCTGTGCAAGACGAGGTTCTGACAGTGCATGACAGTACAGT 335

Qy 80 GluLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyAla 99
 Db 336 GAGAGAAACAAGTACGACGCAAGCCCATTTGATCTTCAAGATGTGACATGATGAGCGCC 395

Qy 100 ThrLeuCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 119
 Db 396 ACCCTGCAATGTGCTTGGAGAGCTGCTGTGATCTTGGGCTCTGGGGAGCAAA 455

Qy 120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerAspGluLeuSerTyrIle 139
 Db 456 CTCATGCCAGCTGCGACAGACTCACTTCAGCTCTTCTGATGAGCTCAAGTGTGATATT 515

Qy 140 GluLeuLeuGluLysAspGlyMetSerPheGlnGluSerLeuGlyAspLeuGlyProPhe 159

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Db      540 GAGCTGCTGAGAGGATGCGATGCGCTTCCAGAGAGCCCTA---GACCCAGGCGCCCTT 596
Qy      160 AAGGAGGlySerProPheAlaGlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyr 179
Db      597 GACCAAGGAGCCCTTTCCTGCGAGAGCTGTCAGACAGTCAGCAAGCCAGCCCTTAC 656
Qy      180 TyrCysSerThrTyrGlyProGlyValAlaProSerProGlySerSerAspValSerThrAla 199
Db      657 CACCCCGGACAGCTGTGGCGAGAGGCCCTCCCTCGGAGAGCTGTGACGCTCCACCGCA 716
Qy      200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeu 219
Db      717 GGGAGCTGTGCTTCTCCGAGACTCCACCTCCTCAGACTCCGATGGAAGTCAGTGGACTG 776
Qy      220 AspLeuThrGluSerLysValAlaPheProArgAspAspPheThrAspTyrLysValGlu 239
Db      777 GATCCCACTATGAGCAAGCTCTTCCCAAGATGCTTTGCTGATCTGCAAGAAAGGGGAT 836
Qy      240 ProLysHisGlyLysArgLysArgGlyLysProArgLysLeuSerLysGlyTyrTrpAsp 259
Db      837 CCCAAGACGCGAAGCGGAAACGAGCGCGGCCCGGAAAGCTGAGCAAAAGTACTGGAC 896
Qy      260 CysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrGluPheIle 279
Db      897 TGTCTCAGAGGCGAAGAGACAGCAAGCGCCCGAGAGCAACCCACTGTGGAGTTTCATC 956
Qy      280 ArgAspIleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTrpGlyLysAsnArgHis 299
Db      957 CGGAGACTCTCTTCCACCGGAGCTCAAGAGGGCTCTATGAAGTGGAGAAATCGGCAT 1016
Qy      300 GlnGlyValPheLysPheLeuArgSerGlyLysAlaValAlaGlnLeuTyrGlyGlnLys 319
Db      1017 GAAGGCGCTTCAAGTCTCGCGCTCGAGAGCTGTGGCCCACTATGGGCGCAAAAGAAA 1076
Qy      320 LysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrLysArg 339
Db      1077 AAGAAACGCAACATGACCTCAGAAAGCTGAGCGGGCCATGAGTCTACTCAAAACGG 1136
Qy      340 GlnIleLeuGlnLysArgValAlaArgLysArgLysLeuValTyrLysPheGlyLysAsnSerSer 359
Db      1137 GAGATCTGGAACGGGTGAGTGGCCGCGAGCTGCTCTACAAAGTTGGCAAAACTCAAGC 1196
Qy      360 GlyTyrLysGlnGlnGlnValGlyGlnSerArgAsn 371
Db      1197 GCGCTGGAAGAGAGAGGTTCTCCAGAGTCGGAAC 1232

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RESULT 4
US-09-964-824A-563
; Sequence 563, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964, 824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236, 033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 028
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 563
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-563

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Alignment Scores:

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Pred. No.: 2,56e-195 Length: 1915
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conservative: 22
Best Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
DB: 9 Gaps: 2

US-08-978-217-16 (1-371) x US-09-964-824A-563 (1-1915)
Qy      1 MetAlaAlaThrCysGlnLysSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
Db      120 ATGGCTGCACACCTGTAGATTAGCAACATTTTACACTACTTCTGATGCTGATGAC 179
Qy      21 SerGluAspProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
Db      180 TCGAGAGACTCCACCTGGCGCTGTGTTCCCTCGTGCACACTTGGGCGCATGACTTG 239
Qy      40 ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGlnGlyProGlnLysValAspTrpHis 59
Db      240 GATCTACACCTGACCAACCCCGAGATGTCATTTGAGAGGTACAGAGAGGCCAGCTGGT 299
Qy      60 SerGluArgProGlnPheTrpSerLysThrGlnValLeuGlnTyrLysSerTrpGlnVal 79
Db      300 GGGGAACAGCCCGACGATTTCTGTGAGAGAGCGAGTTCTGACTGATCAGTACCAAGT 359
Qy      80 GlnLysAsnLysTyrAspAlaSerSerLysAspPheSerArgCysAsnMetAspGlyAla 99
Db      360 GAGAAAGAACAGTACAGCAAGCGCATTTGACTTCTACAGATGTGACATGATGGCGCC 419
Qy      100 ThrLeuCysSerValAlaLeuGlnGlnLysValPheGlyProLeuGlnLysAsnGln 119
Db      420 ACCCTTGCAATGTGCTTCTGAGAGCTGCTGTGCTTTGGGCTCTGGGGAGCCAA 479
Qy      120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGlnLeuSerTrpIleIle 139
Db      480 CTCATGCGCCAGCTGGAGACCTCACTTCCAGTCTTCTGATGAGCTCACTTGATGAT 539
Qy      140 GlnLeuLeuGlnLysAspGlyMetSerPheGlnGlnSerLeuGlnLysLeuGlyProPhe 159
Db      540 GAGCTCTGGAAGAGATGAGCATGGCTTCCAGAGAGCCCTA---GACCCAGGCGCCCTTT 596
Qy      160 AspGlnGlySerProPheAlaGlnGlnLeuLeuAspAspGlyArgGlnAlaSerProTyr 179
Db      597 GACCAAGGAGCCCTTTCCTGCGAGAGCTGTCAGAGAGGTCAGCAAGCCAGCCCTTAC 656
Qy      180 TyrCysSerThrTyrGlyProGlyValAlaProSerProGlySerSerAspValSerThrAla 199
Db      657 CACCCCGGACAGCTGTGGCGAGAGGCCCTCCCTCGGAGAGCTGTGACGCTCCACCGCA 716
Qy      200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeu 219
Db      717 GGGAGCTGTGCTTCTCCGAGACTCCACCTCCTCAGACTCCGATGGAAGTCAAGTGGAC 776
Qy      220 AspLeuThrGluSerLysValAlaPheProArgAspAspPheThrAspTyrLysValGlu 239
Db      777 GATCCCACTATGAGCAAGCTCTTCCCAAGATGCTTTGCTGATCTGCAAGAAAGGGGAT 836
Qy      240 ProLysHisGlyLysArgLysArgGlyLysProArgLysLeuSerLysGlyTyrTrpAsp 259
Db      837 CCCAAGACGCGAAGCGGAAACGAGCGCGGCCCGGAAAGCTGAGCAAAAGTACTGGAC 896
Qy      260 CysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrGluPheIle 279
Db      897 TGTCTCAGAGGCGAAGAGAGCAAGCGCGCCAGAGCAACCCACTGTGGAGTTTCATC 956
Qy      280 ArgAspIleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTrpGlnLysAsnArgHis 299
Db      957 CGGAGACTCTTCAAGTCCACCGGAGCTCAACGAGGCTCATTAAGTGGAGATCGGCAT 1016
Qy      300 GlnGlyValPheLysPheLeuArgSerGlyLysAlaValAlaGlnLeuTyrGlyGlnLys 319
Db      1017 GAAGGCGCTTCAAGTCTCGCGCTCGAGAGCTGTGGCCCACTATGGGCGCAAAAGAAA 1076

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QY 320 LysAsnSerAsnMetThrTyrGluTyrLeuSerArgLametrTyrTyrTyrTyrSarg 339
| | | | |
Db 1077 AAGAACAGCAACTGACCTTACGAGAGCTGACCGGCCCATGAGTACTCTACAAACCG 1136
| | | | |
QY 340 GluIleuGluTyrValArgGlyArgArgLeuValTyrIlePheGlyTyrAsnSerSer 359
| | | | |
Db 1137 GAGATCCTGAGAACGGGTGATGCGCGCGACTGCTCAACAGTTTGGCAAAAACCTCAAGC 1196
| | | | |
QY 360 GlyTyrPheGluGluGluValGlyGluSerArgAsn 371
| | | | |
Db 1197 GGCTGGAGAGGAGAGAGGTTCTCCAGAGTCGGAAC 1232
| | | | |
RESULT 5
US-08-978-107-3420
; Sequence 3420, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3420
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U72843
US-08-978-107-3420
Alignment Scores:
Pred. No.: 2,56e-195 Length: 1915
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conservative: 22
Best Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
DB: Gaps: 2
US-08-978-217-16 (1-371) x US-09-880-107-3420 (1-1915)
QY 1 MetAlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
| | | | |
Db 120 ATGGCTGCAACCTGTGATTTAGCAACATTTTGAACACTTCACTGAGATGTACAGC 179
| | | | |
QY 21 SerGluAspProThrIleuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
| | | | |
Db 180 TCGGAGACTCCACCTCGCTCTGTTCCCTCTCTCTCCACTTTGGGGCCGATGACTTG 239
| | | | |
QY 40 ValIleuThrLeuAsnAngInginMetThrLeuGluGluProGluTyrValAsnSerTyrThr 59
| | | | |
Db 240 GTAAGTACCTGAGCAACCCCAAGATGTCAATTGGAGGTACAGAGAGCCAGCTGGTTG 259
| | | | |
QY 60 SerGluArgProGluPheTyrPheTyrSerTyrThrGluValLeuTyrPheSerTyrGlnVal 79
| | | | |
Db 300 GGGGAAAGCCCACTTGTGTCGACAAACGAGGTTTGGACTGATCAGCTACCAAGTG 359
| | | | |
QY 80 GluTyrAsnTyrTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyVal 99
| | | | |
Db 360 GAGAGAAACAAGTACGACGCAAGCCCATTTCTCAGAGTGTACATGAGAGGCC 419
| | | | |
QY 100 ThrIleuCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 119
| | | | |
Db 420 ACCCTGCAATGTGCTTGAAGAGCTGCTGCTTTTGGGCTCTGGGGAGCAAA 479
| | | | |

QY 120 LeuHISAlaGluLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTyrIlele 139
| | | | |
Db 480 CTCATGCGCCAGCTGGAGAACCTCACTTCCAGCTCTTGTGATGAGCTCATGATCATTT 539
| | | | |
QY 140 GluLeuLeuGluTyrAspGlyMetSerPheGlnGluSerLeuGlyAspLeuGlyProPhe 159
| | | | |
Db 540 GAGCTCCTGAGAGAGATGAGCTGCTTCCAGAGAGCCCTA---GACCAGGCGCTTTT 596
| | | | |
QY 160 AspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyValGlnAlaSerProTyr 179
| | | | |
Db 597 GACCAAGGAGCCCTTGTCCAGAGCTCTTGACAGCAGCTCAGAACCCAGCCCTTAC 656
| | | | |
QY 180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199
| | | | |
Db 657 CACCCGGAGAGCTGTGCGCAGAGAGCCCTCCCTCCGAGCTGTACGTTCCACCGCA 716
| | | | |
QY 200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeu 219
| | | | |
Db 717 GGGACTGTGCTTCTTCGAGAGCTCCCACTCTCAGACTCCGTTGGAGTACGTGACCTG 776
| | | | |
QY 220 AspLeuThrGluSerTyrValPheProArgAspAspPheThrAspTyrIleValGlyIu 239
| | | | |
Db 777 GATCCCACTGATGCGAAGCTCTTCCACGAGTGTTCGTGACTGCAGAAAGGGGGAGT 836
| | | | |
QY 240 ProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerIleGlyTyrTyrAsp 259
| | | | |
Db 837 CCNACACAGGAGAGCGGAAACGAGCCGCGCCCGCAAACTAGCAAAAGTACTGGAGC 896
| | | | |
QY 260 CysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrGluPheIle 279
| | | | |
Db 897 TGTCTGAGGGGCAAGAGAGCAAGCAGCGCCAGAGGACCCACTGTGGAGGTTCATC 956
| | | | |
QY 280 ArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTyrPheGluAsnArgHis 299
| | | | |
Db 957 CGGACATCTTCAAGTCCACCGGAGCTCAAGAGGCTCATGAGTGAAGTGGAGATTCGCAAT 1016
| | | | |
QY 300 GluGlyValPheLysPheLeuArgSerGluAlaValAlaGluLeuTyrPheGlyGlnLys 319
| | | | |
Db 1017 GAAGGCTCTTCAAGTCTCTGCGCTCCGAGGCTGTGGCCCACTAAGGGGCCAAAGAAA 1076
| | | | |
QY 320 LysAsnSerAsnMetThrTyrGluTyrLeuSerArgAlaMetArgTyrTyrTyrSarg 339
| | | | |
Db 1077 AAGAACAGCAACTGACCTTACGAGAGCTGACCGGCCCATGAGTACTCTACAAACCG 1136
| | | | |
QY 340 GluIleuGluTyrValArgGlyArgArgLeuValTyrIlePheGlyTyrAsnSerSer 359
| | | | |
Db 1137 GAGATCCTGAGAACGGGTGATGCGCGCGACTGCTCAACAGTTTGGCAAAAACCTCAAGC 1196
| | | | |
QY 360 GlyTyrPheGluGluGluValGlyGluSerArgAsn 371
| | | | |
Db 1197 GGCTGGAGAGGAGAGAGGTTCTCCAGAGTCGGAAC 1232
| | | | |
RESULT 6
US-09-967-768A-192
; Sequence 192, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatur
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 192
; LENGTH: 1915

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-192

Alignment Scores:
Pred. No.: 2,56e-195      Length: 1915
Score: 1712.00           Matches: 323
Percent Similarity: 92.74%   Conservative: 22
Best Local Similarity: 86.83%  Mismatches: 25
Query Match: 86.25%         Indels: 2
DB: 9                      Gaps: 2

US-08-978-217-16 (1-371) x US-09-967-768A-192 (1-1915)

QY 1 MetAlaIaThrcYsgIuIleSerAsnValPheSerAsnTYrPheAnaIaMeTYrSer 20
DB 120 ATGGCTGCACCTGTGATAGATTAGCAACATTTTAGCACTTCACTGCGATGATACAGC 179
QY 21 SerGIuAspProThrLeuAlaProAlaProPro--ThrThrPheGIyThrGIuAspLeu 39
DB 180 TCGGAGGACTCCACCTGGCTCTGTCTCCCTGCTGCCACCTTTGGGGCCGATGACTTG 239
QY 40 ValLeuThrLeuAsnAnGInGInMetThrLeuGIuGIyProGIuYsAlaSerTPthr 59
DB 240 GTACTGACCTGTAGCAACCCCGAGATGTCAATGGAGGGTACAGAGAGCCAGCTGGTGG 239
QY 60 SerGIuAspProGInPheTrpSerIyThrGInValLeuGIuTrpIleSerTYrGIuVal 79
DB 300 GGGGAACAGCCCGAGTTCTGTGTGAGAACCGAGTTTGGACGTGATGACTACCAAGTG 359
QY 80 GIuLYsAnLYsTYrAspAlaSerSerIleAspPheSerIyGysAsnMetAspGIyAla 99
DB 360 GAGAGAACAGTACGACGACGAGCCGATGACTTCTCAGAGTGTGACATGATGGCGCC 419
QY 100 ThrLeuCYseTYsAlaLeuGIuGIuLeuArgLeuValPheGIyProLeuGIyAspGIn 119
DB 420 ACCCTCTGCATATGTGCTTGTAGAGACTGCTGTGCTTGTGGGCTCTGGGGGACCAA 479
QY 120 LeuHisIaGInLeuArgAspLeuThrSerAsnSerSerAspGIuLeuSerTrpIleIle 139
DB 480 CTCATGTCCAGAGTGGAGACCTCACTTCCAGCTCTTCTATAGAGCTCAATTTGGATATT 539
QY 140 GIuLeuLeuGIuLYsAspGIyMetSerPheGInGIuSerLeuGIyAspLeuGIyProPhe 159
DB 540 GACGCTGTGAGAGAGATGACATGCTCCCTGACAGAGCCCTTA--GACCCAGGGCCCTTT 596
QY 160 AspGIuGIySerProPheAlaGInGIuLeuLeuAspAspGIyArgGInaIaSerProTYr 179
DB 597 GACCAAGGGACGCCCTTGTGCCAGAGACTGTGACAGAGGTCAAGCCAGCCCTTAC 656
QY 180 TYrCYsSerThrTYrGIyProGIyAlaProSerProGIySerSerAspValSerThrAla 199
DB 657 CACCCGGCAGCTGTGCGAGAGAGCCCTCCCTGCGAGCTGTGACGTCTCAACCGCA 716
QY 200 ArgThrAlaThrProGInSerSerHisAlaSerAspSerGIyGIySerAspValAspLeu 219
DB 717 GGAGACTGTGCTCTTCCGAGACTCCCACTCCTCAGACTCCGAGTGAAGTACGTGACCTG 776
QY 220 AspLeuThrGIuSerLYsValPheProArgAspAspPheThrAspTYrLYsLYsGIu 239
DB 777 GATCCCACTATAGCAAGCTCTTCCCAAGCATGTGTTGTGTGCTGCAAGAAAGGGGAT 836
QY 240 ProLYsHisGIyLYsArgLYsArgLYsArgProArgLYsLeuSerLYsGIuTYrTrpAsp 259
DB 837 CCAAGACAGCGGAAGCGGAACAGAGCGCGGCCCGGAAGCTGAGCAAAAGTACTGGAC 896
QY 260 CYsLeuGIuGIyLYsLYsSerLYsHisAlaProArgLYsThrHisLeuTrpGIuPheIle 279
DB 897 TGTCTCGAGGGCAAGAGACAGACAGCGCCCGCAGAGCAACCCAGCTGTGGGAGTTTATC 956
QY 280 ArgAspIleLeuIleHisAspProGIuLeuAsnGIuGIyLeuMetLYsTrpGIuAsnArgHis 299
DB 957 GGGGACATCTCTCAACCCGAGAGCTCAAGAGGGCTCATGAAATGGGAATCGGCAT 1016

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QY 300 GIuGIyValPheLYsPheLeuArgSerGIuAlaValaIaGInLeuTrpGIyGIuLYsLYs 319
DB 1017 GAAGGCGTCTTCAAGTCTTCCTCGCGCTCGAGAGGTGTGGCCCACTATGGGCGCAAAAGAAA 1076
QY 320 LYsAsnSerAsnMetThrTYrGIuLYsLeuSerArgAlaMeCArgTYrTYrTYrLYsArg 339
DB 1077 AAGAACAGCAACATGACCTTACAGAAAGCTGAGCGGGGCATGAGGTACTTACAAACCG 1136
QY 340 GIuIleLeuGIuArgValAspGIyArgArgLeuValTYrLYsPheGIyLYsAsnSerSer 359
DB 1137 GAGATCTCTGGAACGGGTGATGGCCGCGCATCTGTCTTCAAGTTTGGCAAAAATCTAAC 1196
QY 360 GIyTrpLYsGIuGIuGIuValaGIyGIuSerArgAsn 371
DB 1197 GGCTGGAGAGAGAGAGAGGTTCTTCCAGATCGGAGAC 1232

RESULT 7
US-09-922-217-1105
; Sequence 1105, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongrong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121, 471C13
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-1105

Alignment Scores:
Pred. No.: 2,56e-195      Length: 1917
Score: 1712.00           Matches: 323
Percent Similarity: 92.74%   Conservative: 22
Best Local Similarity: 86.83%  Mismatches: 25
Query Match: 86.25%         Indels: 2
DB: 9                      Gaps: 2

US-08-978-217-16 (1-371) x US-09-922-217-1105 (1-1917)

QY 1 MetAlaIaThrcYsgIuIleSerAsnValPheSerAsnTYrPheAnaIaMeTYrSer 20
DB 122 ATGGCTGCACCTGTGATAGATTAGCAACATTTTAGCACTTCACTGCGATGATACAGC 181
QY 21 SerGIuAspProThrLeuAlaProAlaProPro--ThrThrPheGIyThrGIuAspLeu 39
DB 182 TCGGAGGACTCCACCTGGCTCTGTCTCCCTGCTGCCACCTTTGGGGCCGATGACTTG 241
QY 40 ValLeuThrLeuAsnAnGInGInMetThrLeuGIuGIyProGIuYsAlaSerTPthr 59
DB 242 GTACTGACCTGTAGCAACCCCGAGATGTCAATGGAGGGTACAGAGAGCCAGCTGGTGG 301
QY 60 SerGIuAspProGInPheTrpSerIyThrGInValLeuGIuTrpIleSerTYrGIuVal 79
DB 302 GGGGAACAGCCCGAGTTCTGTGTGAGAACCGAGTTTGGACGTGATGACTACCAAGTG 361

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Qy	80	LysAsnLys Tyr Asp Ala Ser Ser Leu Asp Phe Ser Arg Cys Asn Met Asp Glu Val A	99
Db	362	GAGAAAGCAACAGTACGACCAAGCCCACTGACTTCAACAGTACGATGATGATGCCCC	421
Qy	100	Thi Leu Cys Ser Cys Ala Leu Glu Glu Leu Asn Arg Leu Val Phe Gly Pro Leu Gly Asp Gln	119
Db	422	ACCCTCTGCATTTGTGGCTTGTAGGAGGTGGGTCTGTGCTTTGGGCTCTGGGGGACCA	481
Qy	120	Leu H Sa a G In Leu Arg Asp Leu Thi Ser Asn Ser Ser Asp Glu Leu Ser Trp Le le	139
Db	482	CTCCATGCCCGACGTCCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGGATTCATT	541
Qy	140	Glu Leu Leu Glu Lys Asp Gly Met Ser Phe Gln Gln Ser Leu Gly Asp Leu Gly Pro Phe	159
Db	542	GAGCTGCTGGAGAAAGATGGATGGCTTCCAGAGAGGCCCTTA--GACCACAGGGGCTTT	598
Qy	160	Asp Gln Gly Ser Pro Phe Ala Gln Glu Leu Leu Asp Asp Gly Arg Gln Ala Ser Pro Tyr	179
Db	599	GACCAAGGCAACCCCTTTGGCCAGGAGCTGCTGGACAGACGTCACCAAGCCAGCCCCCTAC	658
Qy	180	Tyr Cys Ser Thr Tyr Gly Pro Gly Val Ala Pro Ser Pro Gly Ser Ser Asp Val Ser Thi Ala	199
Db	659	CACCCCGGACACTGGGCGCAGAGAACCCCTCTCCCTGGACAGCTCGAGCTCCACGCCCA	718
Qy	200	Arg Thr Ala Thr Pro Gln Ser Ser Ile Ala Ser Asp Ser Gly Gly Ser Asp Val Asp Leu	219
Db	719	GGGAGCTGGTGCTTCTCGAGAGCTCCACCTCACTCAAGCTCCGGTGAAGATGACGTGGACCTG	778
Qy	220	Asp Leu Thr Glu Ser Lys Val Phe Pro Arg Asp Asp Phe Thr Asp Tyr Lys Lys Glu	239
Db	779	GATCCCACTGATGGCAAGCTCTTCCCAAGCATGTGTTTCTGACTGCAGAGAGGGGAT	838
Qy	240	Pro Lys His Gly Lys Arg Lys Arg Gly Val Arg Pro Arg Lys Leu Ser Lys Glu Trp Asp	259
Db	839	CCCAAGCAGCGGGAAGCGGAACGAGCGCGGCCCGAAGCTGACGAAAGATACCTGGAG	898
Qy	260	Cys Leu Glu Gly Lys Lys Ser Lys His Ala Pro Arg Gly Thr His Leu Trp Lys Phe le	279
Db	899	TGTCCTCGAGGCGCAAGACAGCAGCAGCGCCCAAGGACCCCACTGTGGAGATTCAATC	958
Qy	280	Arg Asp Ile Leu Ile His Pro Glu Leu Asn Gln Glu Lys Met Lys Trp Glu Asn Arg His	299
Db	959	CGGAGCATCTCATCTACCCCGGAGCTCAACGAGGCTCTCATGAGATGGAGATGGCAT	1018
Qy	300	Glu Gly Val Phe Lys Phe Leu Arg Ser Glu Ala Val Ala Gln Leu Trp Gly Gln Lys Lys	319
Db	1019	GAAAGCGCTTCAAGTTCTCTGGCTCCGAGGCTGTGGCCCAACTATGGGGCCAAAGAA	1078
Qy	320	Lys Asn Ser Asn Met Thr Tyr Glu Lys Leu Ser Arg Ala Met Arg Tyr Tyr Tyr Lys Arg	339
Db	1079	AAGAAACAGCAACATGACCTACGACAGAGCTGAGCCGGGCACATGAGGTACTACTACAAACGG	1138
Qy	340	Glu Ile Leu Glu Arg Val Asp Gly Val Arg Arg Leu Val Tyr Lys Phe Gly Lys Asn Ser Ser	359
Db	1139	GAGATCTCGAAGCGGTGTGATGTGGCCGGGACCTGCTCAAGATTGGCAAAATCTCAAGC	1198
Qy	360	Gly Trp Lys Glu Glu Glu Val Gly Glu Ser Arg Asn	371
Db	1199	GGCTGGAGAGAGAGAGAGGTTTCTCCAGAGTCCGAGAC	1234
RESULT 8			
US-10-025-380-1105			
; Sequence 1105, Application US/10025380			
; Publication No. US20020182191A1			
GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Lodes, Michael J.			
; APPLICANT: Secrist, Heather			
; APPLICANT: Benson, Darin R.			
; APPLICANT: Meagher, Madeleine Joy			
; APPLICANT: Stolk, John A.			
; APPLICANT: Wang, Tongrong			
; APPLICANT: Jiang, Yugu			

QY	DB	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
US-08-978-217-16 (1-371) x US-10-025-380-1105 (1-1917)						
QY	1	2.56e-195	Length: 1917			
Db	122	1712.00	Matches: 323			
QY	21	92.74%	Conservative: 22			
Db	182	86.83%	Mismatches: 25			
QY	40	86.25%	Indels: 2			
Db	302	13	Gaps: 2			
QY	60					
Db	362					
QY	100					
Db	422					
QY	120					
Db	482					
QY	140					
Db	542					
QY	160					
Db	599					
QY	180					
Db	659					
QY	200					

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Dh 719 GGAGCTGGTCTTCTCGAGCTCCCACTCCTCAGACTCCGGTGAAGTACGTGGACCTG 778
Qy 220 AspleuThrGluSerIleValPheProArgAspAphPheThrAspTyrIleValGlu 239
Dh 779 GATCCCACTATGGAAGCTCTTCCCAAGCATGTGTTTGTGATCTGCAAGAAAGGGGAT 838
Qy 240 ProluHisGlyIleValArgIleValArgProArgIleuSerIleuValGluTyrTrpAsp 259
Dh 839 CCCAAGACGCGGAAGCGGAACGAGCGCGGCCCGAAGAGCTGAGCAAAAGAGTACTGGAC 898
Qy 260 CylLeuGluGluIleValIleValSerIleValIleProArgIleThrIleuLeuTrpGluPheIle 279
Dh 899 TGCTTCAGAGGCAAGAAAGACACGACGCGCCAGAGGACCCACCTGTGTGGAGTTTATC 958
Qy 280 ArgAspIleleuIleHisProGluLeuAsnGluIleuMetIleValTrpGluAsnArgHis 299
Dh 959 CGGGACATCTTCATCCACCGGAGCTCAACGAGGCTTCATGAAGTGGAGAAATCGGCAT 1018
Qy 300 GluGlyValPheIleValPheLeuArgSerGluIleValIleGluLeuTrpGluIleValIle 319
Dh 1019 GAAGGCGCTTCAAGATTCTGCGCTCCGAGGCTGTGGCCCAACTATGGGCGCAAAAGAAA 1078
Qy 320 LysAsnSerAsnMetThrTyrGluValLeuSerArgIleMetArgTyrTyrTyrIleValArg 339
Dh 1079 AAGAACAAGCAACATGACTACGAGAACTGAGCCGGCCATGAGATCTACTCAAAACGG 1138
Qy 340 GluIleleuGluValArgValAspGlyArgArgLeuValTyrIlePheGlyIleAsnSerSer 359
Dh 1139 GAGATCTGGAACCGGTGATGGCGCGGCACTGCTTACAAAGTTTGGCAAAACTCAAGC 1198
Qy 360 GlyTyrIleGluGluGluValIleGluIleuSerArgAsn 371
Dh 1199 GGCTGGAAAGAGAGAGAGGTTCTCCAGAGTCGGAAC 1234

RESULT 9
US-10-264-049-756
; Sequence 756, Application US/10264049
; Publication No. US2004000579A1
; GENERAL INFORMATION:
; APPLICANT: Birsse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P133P1
; CURRENT APPLICATION NUMBER: US/10/264, 049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 756
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-264-049-756

Alignment Scores:
Pred. No.: 2,64e-195 Length: 1956
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conserved: 22
Best Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
Gaps: 2

US-08-978-217-16 (1-371) x US-10-264-049-756 (1-1956)
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Qy 40 ValIleuThrLeuAsnAsnGluGluIleMetThrLeuGluIleProGluIleValIleSerTrpThr 59
Dh 281 GTACTGACCTGTGAGCAACCCCAAGATGTCATTGGAGGATACAGAAAGCCAGCTGTTG 340
Qy 60 SerGluArgProGluInPheTrpSerIleValIleGluTrpIleSerTyrGluVal 79
Dh 341 GGGAAACAGCCCAAGTTCTGTGTGGAAGACGAGGTTCTGATGATGATCAACCAAGTG 400
Qy 80 GluIleAsnIleValIleAspIleAspSerIleAspPheSerArgCysAsnMetAspGlyAla 99
Dh 401 GAGAAACAAGTACACACGCAAGCCCATTTGACTTCTACGATGTACATGATGAGCGCC 460
Qy 100 ThrLeuCysSerCysAlaIleuGluGluIleuValArgLeuValPheGlyProleuGlyAspGlu 119
Dh 461 ACCCTCTGCAATGTGCTCCCTTGAAGAGCTGCGTCTGCTCTTGGGCTCTGGGGAGACAA 520
Qy 120 LeuHisAlaGluLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIle 139
Dh 521 CTCATGCCCAGCTGGAGAACCTCACTTCAAGCTTCTGATGAGCTCAAGTTGGATCAAT 580
Qy 140 GluLeuLeuGluIleValAspGlyMetSerPheGluIleuSerIleuValAspLeuGlyProPhe 159
Dh 581 GACTCTGTGAGAAAGATGATGATGCTTCCAGAGGCTCTA---GACCCAGGCTCTT 637
Qy 160 AspGluGlySerProPheAlaGluGluIleuLeuAspAspGlyArgGluIleAspProTyr 179
Dh 638 GACCAAGGAGCCCTTTGCTCCAGAGCTGTGAGACGATGACGACCAAGCCCTCA 697
Qy 180 TyrCysSerThrTyrIleProGlyAlaProSerProGlyIleSerSerAspValSerThrAla 199
Dh 698 CACCCGCGGACGCTGTGCGCAAGAGCCCTTCCCTCGGAGCTCTGACCTTCCACCGGA 757
Qy 200 ArgThrAlaThrProGluInSerSerHisAlaSerAspSerGlyIleSerAspValAspLeu 219
Dh 758 GGGACTGTGCTCTTCTCGAGCTCCCACTCTCAAGATCCGGTGAAGTACGTGACCTG 817
Qy 220 AspleuThrGluSerIleValPheProArgAspAphPheThrAspTyrIleValGlu 239
Dh 818 GATCCCACTGATGGAAGCTCTTCCCAAGCATGTGTTTCGTGACTGCAAAAGGGGGAT 877
Qy 240 ProluHisGlyIleValArgIleValArgProArgIleuLeuSerIleuValIleTrpAsp 259
Dh 878 CCCAACAAGCGGAAGGGGAACGAGGCGCGCCCGAAGCTGAGCAAAAGATCTGGGAC 937
Qy 260 CylLeuGluGlyIleValSerIleValIleProArgGlyThrHisleuTrpGluPheIle 279
Dh 938 TGCTTCAGAGGCAAGAAAGCAAGCAAGCGGCCCAAGGCAACCACTGTGGAGTTTATC 997
Qy 280 ArgAspIleleuIleHisProGluLeuAsnGluIleuMetIleValTrpGluAsnArgHis 299
Dh 998 CGGACATCTCTCATCCACCGGAGCTTAAAGAGGCGCTATGAAAGTGGAGAAATCGCAT 1057
Qy 300 GluGlyValPheIleValPheLeuArgSerGluIleValIleGluLeuTrpGluIleValIle 319
Dh 1058 GAAGGCGCTTCAAGTTCTGCGGTCCGAGGCTGTGGCCCAACTATGGGCGCAAAAGAAA 1117
Qy 320 LysAsnSerAsnMetThrTyrGluValLeuSerArgAlaMetArgTyrTyrTyrIleValArg 339
Dh 1118 AAGAACAAGCAACATGACTACGAGAACTGAGACCGGCCCATGAGATCTACTCAAAACGG 1177
Qy 340 GluIleleuGluValArgValAspGlyArgArgLeuValTyrIlePheGlyIleAsnSerSer 359
Dh 1178 GAGATCTGGAACCGGTGATGGCGCGGCACTGCTTCAAAAGTTTGGCAAAACTCAAGC 1237
Qy 360 GlyTyrIleGluGluGluValIleGluIleuSerArgAsn 371
Dh 1238 GGCTGGAAGAGAGAGAGGTTCTCCAGAGTCGGAAC 1273

RESULT 10
US-09-925-301-207
; Sequence 207, Application US/09925301
; Patent No. US20020052308A1
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 207
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-301-207

Alignment Scores:
Pred. No.: 2,72e-195 Length: 1996
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conservative: 22
Best Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
DB: Gaps: 2

US-08-978-217-16 (1-371) x US-09-925-301-207 (1-1996)
QY 1 MetAlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
Db 141 ATGGCTGCAACCTGTGATTAGCAACATTTTAGCACTTACAGTGTGATGATGACAGC 200
QY 21 SerGluAspProThrIleuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
Db 201 TCGGAGACCTCCACCCCTGCTGTTCCCTGCTGCCACCTTTGGGCGCATGACTTG 260
QY 40 ValIleuThrIleuAsnEngInMetThrIleuGluGlyProGluYsaIleSerTrpThr 59
Db 261 GTTCTGACCTTGAGCAACCCCGAGATGCTTTGGAGGTTACAGAGAGCCAGCTGGTTG 320
QY 60 SerGluArgProGlnPheTrpSerTyrThrGlnValIleuGluTrpIleSerTyrGlnVal 79
Db 321 GGGGAAACGCCAGGTTCTGTGAGAGACGAGGTTCTGAGTGTGATGATCACTCAAGTG 380
QY 80 GluIleAsnLysTyrIleAspAlaSerSerIleAspPheSerArgCysAsnMetAlaGlyAla 99
Db 381 GAGAGAAACAGTACGACGAGAGCCATTCAGTCTTCAGAGATGACATGATGGGCC 440
QY 100 ThrIleuCysSerCysAlaIleuGluGluIleuArgIleuValPheGlyProIleuGlyAspGln 119
Db 441 ACCCTCTGCAATTGTGCTTGGAGAGCTGCTGTCTTTGGGCTCTGGGGACCAA 500
QY 120 LeuHisAlaGlnIleuArgAspLeuThrSerAsnSerSerAspGluIleuSerTrpIleIle 139
Db 501 CTCACAGCCAGCTGCGAGACCTTCATTCAGCTCTTCATGATGATGATGATGATCAT 560
QY 140 GluIleuGluGluYsaGlyMetSerPheGlnGluSerIleuGluAspLeuGlyProPhe 159
Db 561 GAGCTGCTGAGAGAGATGCGATGCGCTTCAGAGAGCCCTA--GACCCAGAGGCCCTTT 617
QY 160 AspGlnGlySerProPheAlaGlnGluIleuAspAspGlyArgGlnAlaSerProTyr 179
Db 618 GACACGGGAGCCCTTTGCTCCAGAGCTGTGACACAGTACAGCAAGCCAGCCCTTAC 677
QY 180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValIleSerThrAla 199
Db 678 CACCCCGGAGCTGTGCGAGAGAGGCCCTCCCTCCGAGCTGACGCTCCACCGCA 737
QY 200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeu 219
Db 738 GGGAGCTGTGCTTCTCGAGCTCCCATCTCAACCTCCGATGAAATGACGTGGACCTG 797
QY 220 AspLeuThrGluSerLysValPheProArgAspAspPheThrAspTyrLysLysGlyGlu 239

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Db 798 GATCCACAGTATGCGAAGCTCTTCCCGAGCATGGTTTCTGACTGCAAGAGGGGGAT 857
QY 240 ProLysHisGlyLysArgLysArgLysArgProArgLysLeuSerLysGluTrpAsp 259
Db 858 CCCAAGCAGGGAGAGGAGGAAAGAGAGCCGGCCCAAGAGCTAGAGAAAGATAGGGAG 917
QY 260 CysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIle 279
Db 918 TGTCTGAGGGGCAAGAGAGCAAGCAGCGGCCCAAGAGCAACCACTGTGGAGTTCAATC 977
QY 280 ArgAspIleLeuIleHisProGluIleuAsnGluGlyLeuMetLysTrpGluAsnArgHis 299
Db 978 CCGAGACATCTCATCCACCCGAGCTCAACGAGGCTCATAGAGTGAAGATGCGCAT 1037
QY 300 GluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLys 319
Db 1038 GAAGGCTTCAAGTCTGCTCGAGGCTGAGGCTCAATGAGGCGCAAAAGAA 1097
QY 320 LysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrLysArg 339
Db 1098 AAGAACGAAATACATGACCTACAGAGAGCTGAGCCGCGCATGAGTACTACTCAAAACG 1157
QY 340 GluIleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSer 359
Db 1158 GAGATCTGGAACGGGTGATGCGCGGCACTGCTTCAAGATTGGCAAAATCAACAGC 1217
QY 360 GlyTrpLysGluGluGluValGlyLysSerArgAsn 371
Db 1218 GGCTGGAGAGAGAGAGGTTCTCCAGATCGGAAC 1253

RESULT 11
US-10-131-410-64
; Sequence 64, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPEECH, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKI, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; TITLE OF INVENTION: TUMORS
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-410-64

Alignment Scores:
Pred. No.: 1,05e-164 Length: 2269
Score: 1458.50 Matches: 281
Percent Similarity: 93.71% Conservative: 17
Best Local Similarity: 88.36% Mismatches: 19
Query Match: 73.48% Indels: 3
DB: Gaps: 1

US-08-978-217-16 (1-371) x US-10-131-410-64 (1-2269)
QY 54 GluIleYsaIleSerTrpThrSerGluArgProGlnPheTrpSerLysThrGlnValIleGlu 73
Db 15 GAGAAAGCAGCTGTGGTGGGAAACGCCAGTCTGTGTGAAAGG-CAGGTTCTGAC 73

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Qy	7	TriplaserYrGlnValGulYsaAnLrYrAspAlaserSerIlAspPheSerArg	93
Db	74	TGgATCAGCTACCAAGTGGAGGAAGAACAAATGACAGCAAGGCCATGATCTTCACGA	133
Qy	94	CyabAmrArspGlyAlaThrIleuCySerCySalAlaLeuGluLeuArgLeuValPhe	113
Db	134	TGTGACATGTAGTGGCGCACCCCTCTCCAAATTGGCCCTTGGAGAACTCCGCTGTCTTT	193
Qy	114	GIProleuGIYArpGlnIleuNH2SalAGlnLeuArgArpLeuThrSerAsnSerSerAsp	133
Db	194	GGGCTCTGGGGAGAACACTCCATGCCCAAGCTTGCGAGACTTCACTTCCAGCTTCTGAT	253
Qy	134	GluLeuSerTripleIleGluLeuLeuGluYAspGlyMetSerPheGlnGluSerIleu	153
Db	254	GAGCTCAGTTGATCATTTGAGCTGTCTGAGAAAGATGGCATGGCTCTTCAGAGAGCCCTA	313
Qy	154	GIYArpLeuGluProPheArpGlnGlySerSerProPheAlaGlnGluLeuLeuArpGly	173
Db	314	--GACCCAGGCGCCCTTTGACAGGGGACACCCCTTTGGCCAGAACTCTGACAGCGGT	370
Qy	174	ArgGlnAlaSerProTYrTYrCySerThrTYrGlyProGluYAlaProSerProGlySer	193
Db	371	CAGCAACCCAGCCCTTACCAACCCCGGCACTGTGGCGCAGAGAGCCCTCCCTCTGGACG	433
Qy	194	SerArpValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGly	213
Db	431	TCTGACCTTCCACCGC-AGGACTGTGTCTTCGGAGCTCCCACTCTCCAGACTCCGGT	489
Qy	214	GIYSerArpValArpLeuArpLeuThrGluSerIleValPheProArgAspArpPheThr	233
Db	490	GGAGTACCTGACCTCGATCCCATCTAGTGGCAAGCTTTCCCAAGGATGGTTTCGT	549
Qy	234	AspTYrIleYAspGlyGluProIleYAspGlyYAspGlyYAspGlyYAspGlyYAsp	253
Db	550	GACTGCAGAGAGGGGGGTCCCAAGCAGGGAAAGCGGAAACGAGCGGCGCCGAAAGCTG	609
Qy	254	SerIleGluTYrThrArpCyIleuGlnGluYIleYAspSerIleAlaProArgGlyThr	273
Db	610	AGCAAAAGATGCTGGGCTCTCTCGAGGGCAAGAAAGCAAGCAAGCCGCCCAAGGACCC	669
Qy	274	HisLeuTrpGluPheIleArpAlaLeuIleHisArpGluLeuAsnGluYLeuMet	293
Db	670	CACCTGTGGAGTTCATCCGGGACATCTCATTCACCCGAACTCAAGAGGGCTCATG	723
Qy	294	LYsTrpGluAsnArgHisGluGluYAlaPheIlePheLeuArgSerGluYAlaIleGln	313
Db	730	AAGGGGAGAGATCGGCATGAAAGCGCTTCAAGTTCTCGCTCCGAGCGTGTGGCCAA	789
Qy	314	LeuTrpGluGlnIleYAspIleAsnSerAsnMetThrTYrGluYLeuSerArgAlaMet	333
Db	790	CTATGGGGCCAAAAGAAAAGAACACAACTGACTTACAGAACTAGACCCGGGCATG	849
Qy	334	ArgTYrTYrTYrIleYAspArgGluIleLeuGluArgValAspGlyArgArgLeuValTYrIle	353
Db	850	AGGACTACTACAAACCGGAGAGCTCTGGAACGGGTGATGTGCGCGGACTGTCTACAG	909
Qy	354	PheGluYAspAsnSerSerGlyTYrTrpIleGlnGluGluYAlaGluYLeuSerArgAsn	371
Db	910	TTTGGCAAAAATCAGCGGCTGGAAAGAGAGAGAGTTCTTCAGAGTGGAGAC	963
RESULT 12			
US-09-922-217-853/c			
; Sequence 853, Application US/09922217			
; Patent No. US20020076414A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiequn			
; APPLICANT: Lodes, Michael J.			
; APPLICANT: Secretic, Heather			
; APPLICANT: Benson, Darin R.			
; APPLICANT: Meagher, Madeleine Joy			
; APPLICANT: Stolk, John A.			
; APPLICANT: Wang, Tongcong			
; APPLICANT: Jiang, Yugu			

	APPLICANT:	Smith, Carole Lynn	
	APPLICANT:	King, Gordon E.	
	APPLICANT:	Mang, Ajjun	
	APPLICANT:	Clapper, Jonathan D.	
	TITLE OF INVENTION:	COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS	
	TITLE OF INVENTION:	OF COLON CANCER AND METHODS FOR THEIR USE	
	FILE REFERENCE:	210121.471C13	
	CURRENT APPLICATION NUMBER:	US/09/922,217	
	CURRENT FILING DATE:	2001-08-03	
	NUMBER OF SEQ. ID NOS:	1124	
	SOFTWARE:	FastsEQ for Windows Version 4.0	
	SEQ ID NO 853		
	LENGTH:	626	
	TYPE:	DNA	
	ORGANISM:	Homo sapiens	
/	US-09-922-217-853		
Alignment Scores:			
Pred. No.:	9.88e-102	Length:	626
Score:	928.50	Matches:	174
Percent Similarity:	90.91%	Conservative:	16
Best Local Similarity:	83.25%	Mismatches:	18
Query Match:	46.78%	Indels:	1
DB:	9	Gaps:	1
US-08-978-217-16 (1-371) x US-09-922-217-853 (1-626)			
Qy	52	GlyProGluIuLyAlaSerTrpThrSerGluArgProGlnPheTrpSerLysThrGlnVal	71
Db	624	GGTAACAGAAAGGCCAGCTGTGGTGGGGGAACAGCCCACTTCCTGGTCGAAGCGCAGGTT	56
Qy	72	LeuGluTrpLleSerTrpGlnValGluLysAsnLysTrpAspAlaSerSerLleAspHe	91
Db	564	CTGAGACTGATTCAGCTAACAGTGAGAAGAACAACTAAGACGACCAAGCCCATTAATTTC	50
Qy	92	SerArgCyseAmMetAspGlyAlaThrLysCysSerCysAlaLeuGluGluLysuArgLeu	11
Db	504	TACAGATGACATGATGATGGCCGCACCTCTGCATATGTGGCTTAGAGAGCTGGCTCG	44
Qy	112	ValPheGluProLeuGluLysArgLnuEuhIaIaGlnLnuArgAspLnuThrsSerAnsEr	13
Db	444	GTCCTTGGGCTCTGGGGGACCMAACTCCATGCCACGCTCGAGACTTCCTCCAGCTCT	38
Qy	132	SerAspGluLnuSerTrpLleIleGluLnuLauGluLysAspGlyMetSerPheGlnGlu	15
Db	384	TCGATGAGCTCACTTGATGATCATGTAGCTGTGGAGAAAGATGGACCTTCCAGAG	32
Qy	152	SerLeuGlyAspLnuGlyProPheAspGlnGlySerProPheAlaGlnGluLnuLnuAsp	17
Db	324	GGCCTA---GACCCAGAGGCCCTTTGACAGGGGAGGCCCTTTGGCCAGAGCTGTGGAC	26
Qy	172	AspGlyArgGlnAlaSerProTrpTrpCysSerThrTrpGlyProGlyValaProSerPro	19
Db	267	GAGGGTCAGCAACCCAGCCCCCTAACCCCGGACGCTGGGGCAGAGACCCCCTTCCCC	20
Qy	192	GlySerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAsp	21
Db	207	GGCAGCTTCAGCTCTCCACCGAGGGAATGGCTTCTTCGAGAGCTCCACACTCCACAGC	14
Qy	212	SerGlyGlySerAspValAspLnuAspLnuThrGlnLysErLysValaPheProArgAspAsp	23
Db	147	TCCGGTGAAGTACCTGAGACCTCGATCCACACTGATGGGCAACCTCTTCCCCGCGATGAT	88
Qy	232	PheThrAspTrpTrpLysGlyGluProLysHISgLYLAArgLysArgGlyArgProArg	25
Db	87	TTTCGTGACTGCAGAAAGGGGGATCCCAAGCACGGGAAACGGAAACGAGCCGCCCGGA	28
Qy	252	LysLeuSerLysGluTrpTrpAspCys	260
Db	27	AAGCTGAGCAAAGATAGTACTGGAGCTGT	1


```
; Sequence 853, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-833-263-853

Alignment Scores:
Pred. No.: 9.88e-102 Length: 626
Score: 928.50 Matches: 174
Percent Similarity: 90.91% Conservative: 16
Best Local Similarity: 83.25% Mismatches: 18
Query Match: 46.78% Indels: 1
DB: 9 Gaps: 1

US-08-978-217-16 (1-371) x US-09-833-263-853 (1-626)
Qy 52 GlyProGluLysAlaSerTrpThrSerGluArgProGlnPheTrpSerIleThrGlnVal 71
Db 624 GGTACAGAGAGAGGCGACGCTGTTGGGGAGACGCCCACTTCTGTCGAGACCCAGCTT 565
Qy 72 LeuGluTrpIleSerTrpGlnValGluLysAsnLysTrpAlaSerSerIleAspPhe 91
Db 564 CTGACCTGAGTCAAGCTACCAAGTGAAGAGAACAGTACGCAACGCCGACATTGACTTC 505
Qy 92 SerArgCysAsnMetAspGluAlaThrLeuCysSerCysAlaLeuGluGluLeuArgLeu 111
Db 504 TCACGATGTACAGATGATGGGCGACCCCTGCAATTGTGCTTGAGAGCTGGCTG 445
Qy 112 ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSer 131
Db 444 GTCTTTGGGCTCTGGGGGAGCAACTCCATGCCAGCTCCGACCTCCACTTCAGCTCT 385
Qy 132 SerAspGluLeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetSerPheGlnGlu 151
Db 384 TCTGATGAGCTCAAGTTGATGATCATTTGAGCTGCGAGAGATGGCATGGCTTCAGAG 325
Qy 152 SerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAsp 171
Db 324 GCCCTA---GACCCAGGGCCCTTTGACAGAGGCGCCCTTTGGCCAGAGCTGCTGAC 268
Qy 172 AspGlyArgGlnAlaSerProIleTrpCysSerThrTrpArgIleProGlyAlaProSerPro 191
Db 267 GACGCTAGCAGACGACGACCCCTTACACCCCGGACGCTGTGGCGAGAGCCCTCCCTCC 208
Qy 192 GlySerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAsp 211
Db 207 GGCAGCTCTACAGCTCTCCACCGCAGGAGCTGTGCTCTCCGAGCTCCCACTCTCAGAC 148
Qy 212 SerGlyGlySerAspValAspLeuAspLeuThrGlnSerIleValPheProArgAspAsp 231
Db 147 TCCGCTGAGAGTGCAGTGACCTGATCCCACTATGCAAGCTCTTCCCAAGGATGT 88
Qy 232 PheThrAspTrpLysGlyGluProLysHisGlyLysArgLysArgGlyArgProArg 251
Db 87 TTTCGTATCATCCAGAGAGGGGAGATCCCAAGCAGCGGAGAGACGAGAGGCCGCCCA 28
Qy 252 LysLeuSerLysGlyTrpAspCys 260
Db 27 AAGCTGAGCAAAAGAGTACTGGGACTGT 1
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RESULT 14
US-10-025-380-853/C
; Sequence 853, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Benson, Heather
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 853
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-025-380-853

Alignment Scores:
Pred. No.: 9.88e-102 Length: 626
Score: 928.50 Matches: 174
Percent Similarity: 90.91% Conservative: 16
Best Local Similarity: 83.25% Mismatches: 18
Query Match: 46.78% Indels: 1
DB: 13 Gaps: 1

US-08-978-217-16 (1-371) x US-10-025-380-853 (1-626)
Qy 52 GlyProGluLysAlaSerTrpThrSerGluArgProGlnPheTrpSerIleThrGlnVal 71
Db 624 GGTACAGAGAGAGGCGACGCTGTTGGGGAGACGCCCACTTCTGTCGAGACCCAGCTT 565
Qy 72 LeuGluTrpIleSerTrpGlnValGluLysAsnLysTrpAlaSerSerIleAspPhe 91
Db 564 CTGACCTGAGTCAAGCTACCAAGTGAAGAGAACAGTACGCAACGCCGACATTGACTTC 505
Qy 92 SerArgCysAsnMetAspGluAlaThrLeuCysSerCysAlaLeuGluGluLeuArgLeu 111
Db 504 TCACGATGTACAGATGATGGGCGACCCCTGCAATTGTGCTTGAGAGCTGGCTG 445
Qy 112 ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSer 131
Db 444 GTCTTTGGGCTCTGGGGGAGCAACTCCATGCCAGCTCCGAGACTCCACTCTCAGCTCT 385
Qy 132 SerAspGluLeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetSerPheGlnGlu 151
Db 384 TCTGATGAGCTCAAGTTGATGATCATTTGAGCTGCGAGAGATGGCATGGCTTCAGAG 325
Qy 152 SerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAsp 171
Db 324 GCCCTA---GACCCAGGGCCCTTTGACAGAGGCGCCCTTTGGCCAGAGCTGCTGAC 268
Qy 172 AspGlyArgGlnAlaSerProIleTrpCysSerThrTrpArgIleProGlyAlaProSerPro 191
Db 267 GACGCTAGCAGACGACCCCTTACACCCCGGACGCTGTGGCGAGAGCCCTCCCTCCCTCC 208
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QY 192 GlySerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAsp 211
Db 207 GGCAGCTCTGACGCTCCACCGGAGGAGCTGCTCTTCTCGAGCTCCACTCCTCGAC 148
QY 212 SerGlyGlySerAspValAspLeuAspLeuThrGlnSerLysValPheProArgAsp 231
Db 147 TCCGGTGAAGTACGCGGACCTGGATCCACTGATGCAAGCTCTTCCCGCATGGT 88
QY 232 PheThrAspTyrLysLysGlyGluProLysHisGlyLysArgLysArgGlyArgProArg 251
Db 87 TTTCGTGACTGCAAGAAAGGGGAGATCCCAAGCAGCGGAAGCGAAACAGAGCCGGCCCGA 28
QY 252 LysLeuSerLysGlyTyrTrpAspCys 260
Db 27 AACCTGAGCAAGAGTACTGGGACTGT 1

RESULT 15
US-09-922-217-944/C
; Sequence 944, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodee, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Jiang, Yugui
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922.217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PaateSeq for Windows Version 4.0
; SEQ ID NO 944
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-944

Alignment Scores:
Pred. No.: 2,29e-90 Length: 563
Score: 833.50 Matches: 157
Percent Similarity: 91.49% Conservative: 15
Best Local Similarity: 83.51% Mismatches: 15
Query Match: 41.99% Indels: 1
DB: 9 Gaps: 1

US-08-978-217-16 (1-371) x US-09-922-217-944 (1-563)
QY 73 GluTrpLysSerTyrGlnValGluLysAsnLysTyrAspAlaSerSerIleAspPheSer 92
Db 562 GACTGATCAGCTACCAAGTGAAGAAAGAACAGTACGACCAAGCGCATTTGACTTCTCA 503
QY 93 ArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluGluLeuArgLeuVal 112
Db 502 CGATGTGACATGATGCGCGCACCTCTGCATTTGCTCCCTTGAGGAGCTGCGTGGTC 443
QY 113 PheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSer 132
Db 442 TTGGGGCTCTGGGGGACCACTCCATGCGCAGCTGCGAGACCTTCACCTTCAGCTCTTCT 383
QY 133 AspGluLeuSerTrpLysLysGluLeuLeuGluLysAspGlyMetSerPheGlnGluSer 152
Db 382 GATGAGCTCAGTTGATGATCTTGAAGCTGCTGGAAGAAGATGCGATGCGCTTCCAGAGGCC 323
QY 153 LeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAsp 172

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Db 322 CTA---GACCCAGGGCCCTTTGACACAGGCGAGCCCTTTGCCAGAGCTGCTGACGAC 266
QY 173 GlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyValAspProSerProGly 192
Db 265 GGTACAGAACCCAGCCCCCTACACCCCCGACGCTGGGCGCAGAGCCCCCTTCCCCGAC 206
QY 193 SerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSer 212
Db 205 AGCTTGACGTCTCCACCGCAGGAGCTGGTGTCTTCGAGAGCTCCCACTCTCAAGACTCC 146
QY 213 GlyGlySerAspValAspLeuAspLeuThrGlnSerLysValPheProArgAspPhe 232
Db 145 GGTGAAGTGAAGCTGACCTGATCCCACTGATGCGCAAGCTCTTCCCGCATGGTGT 86
QY 233 ThrAspTyrLysLysGlyGluProLysHisGlyLysArgLysArgGlyArgProArgLys 252
Db 85 CGTGACTGCAAGAAAGGGGAGATCCCAAGCAGCGGAAGCGAAACAGAGCCGGCCCGAAG 26
QY 253 LeuSerLysGluTyrTrpAspCys 260
Db 25 CTGAGCAAGAGTACTGGGACTGT 2

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Job time : 637.855 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 14:00:59 ; Search time 114.561 Seconds
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Perfect score: 1985
Sequence: 1 MATCEISNVFNFMNAMS.....YKFGKNSGCKEKEVEGSRN 371

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Deloext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1712	86.2	1907	4	US-09-300-958A-27
2	1712	86.2	1907	4	US-09-570-593-4
3	1712	86.2	1920	1	US-08-746-789A-1
4	803	40.5	502	4	US-09-389-681-282
5	803	40.5	502	4	US-09-620-405B-282
6	803	40.5	502	4	US-09-339-338-282
7	803	40.5	502	4	US-09-433-826B-282
8	803	40.5	502	4	US-09-604-287A-282
9	803	40.5	502	4	US-09-834-759-282
10	803	40.5	502	4	US-09-590-751A-282
11	586	29.2	5427	3	US-09-009-913-2
12	580	29.2	5510	3	US-09-009-913-3

13	580	29.2	5667	3	US-09-009-913-4	Sequence 4, Appli
14	543	27.4	852	3	US-09-020-956-44	Sequence 44, Appl
15	543	27.4	852	3	US-09-030-607-44	Sequence 44, Appl
16	543	27.4	852	3	US-09-439-313-44	Sequence 44, Appl
17	543	27.4	852	3	US-09-352-616A-44	Sequence 44, Appl
18	543	27.4	852	4	US-09-232-149A-44	Sequence 44, Appl
19	543	27.4	852	4	US-09-159-812-44	Sequence 44, Appl
20	543	27.4	852	4	US-09-636-215-44	Sequence 44, Appl
21	543	27.4	852	4	US-09-685-166A-44	Sequence 44, Appl
22	543	27.4	852	4	US-09-115-453-44	Sequence 44, Appl
23	543	27.4	852	4	US-09-688-489-44	Sequence 44, Appl
24	543	27.4	852	4	US-09-679-426-44	Sequence 44, Appl
25	507	25.5	848	3	US-09-009-913-338	Sequence 338, App
26	435.5	21.9	2280	3	US-09-009-913-6	Sequence 6, Appli
27	435.5	21.9	2498	3	US-09-016-434-927	Sequence 927, App
28	435.5	21.9	237	4	US-09-368-281-1	Sequence 1, Appli
29	238.5	12.0	2375	1	US-08-368-281-3	Sequence 1, Appli
30	238.5	12.0	3240	1	US-08-368-281-3	Sequence 3, Appli
31	238.5	12.0	1528	3	US-08-878-177-3	Sequence 3, Appli
32	234.5	11.8	1894	4	US-09-570-593-1	Sequence 1, Appli
33	233.5	11.8	1905	3	US-09-055-113-2	Sequence 2, Appli
34	233.5	11.8	3317	4	US-09-570-593-12	Sequence 12, Appl
35	233.5	11.8	1604	1	US-08-306-691B-43	Sequence 43, Appl
36	225.5	11.4	1604	5	PCT-US93-06251-9	Sequence 9, Appli
37	225.5	11.4	1447	3	US-08-878-177-1	Sequence 1, Appli
38	225	11.3	2938	2	US-08-343-443B-3	Sequence 3, Appli
39	225	11.3	2268	3	US-09-344-579-1	Sequence 1, Appli
40	220	11.1	1752	3	US-09-360-779-1	Sequence 1, Appli
41	214	10.8	1752	3	US-09-435-335-1	Sequence 1, Appli
42	214	10.8	1933	4	US-09-920-759-3	Sequence 3, Appli
43	214	10.8	1933	4	US-09-920-759-10	Sequence 10, Appl
44	214	10.8	1976	4	US-09-270-767-10903	Sequence 10903, A
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ALIGNMENTS

RESULT 1
US-09-300-958A-27
; Sequence 27, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welch, John
; APPLICANT: Trentle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 27
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-300-958A-27

Alignment Scores:
Pred. No.: 6,79e-177
Score: 1712.00
Percent Similarity: 92.74%
Best Local Similarity: 86.83%
Query Match: 86.25%
DB: 4
Gaps: 2
Length: 1907
Matches: 323
Conservative: 22
Mismatch: 25
Indels: 2
US-08-978-217-16 (1-371) x US-09-300-958A-27 (1-1907)

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QY 1 MetAlaIaThrCysGluIleSerAsnValPheSerAsnTyPheAsnAlaMetTySer 20
Db 96 ATGGCTCAACCTGTGAGATTAGCAACATTTTAGCAACTCTTCAGTGCATGTACAGC 155
QY 21 SerGluAspProThrIleuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
Db 156 TCGGAGAGACTCCACCTGGCTCTGTTTCCCTCTCTCCACCTTTGGGCGGAGACTTG 215
QY 40 ValIeuThrIleuAsnAngInglMetThrIleuGluGlyProGluValAspSerTrpThr 59
Db 216 GTACTGACCTTGAGCAACCCCAATGTCAATTGAGGAGTACAGAGAGGCGGAGCTGGT 275
QY 60 SerGluArgProGlnPheTrpSerLeuThrGlnValIleuGluTrpIleSerTyGlnVal 79
Db 276 GGGGAGACAGCCCGAGTCTGGTTCAGAGCGAGGTTCTGAGCTGATCAGTACCAAGTG 335
QY 80 GluIleAsnIleTyTrpAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyVal 99
Db 336 GAGAGAGAACAGTACGACGAGCGCAATGACTTTCACAGATGTGACATGATGGCGCC 395
QY 100 ThrIleuCysSerCysAlaIleuGluGluIleuArgLeuValPheGlyProIleuGluAspGln 119
Db 396 ACCCTCTGCATTTGTGCTTGGAGAGCTGCTGCTGCTTGGGCTCTGGGAGACCAA 455
QY 120 LeuHisAlaGlnIleuArgAspLeuThrSerAsnSerAspGluIleuSerTrpIleIle 139
Db 456 CTCATGCTCCAGCTGCGAGACCTCACTTCAGCTCTTCTGATGAGTCACTGATGATCAT 515
QY 140 GluIleuIleuGluValAspGlyMetSerPheGlnIleuSerLeuGluValAspLeuGlyProPhe 159
Db 516 GAGCTGCTGAGAGAGATGAGTGCATGCTTCCAGAGAGCCCTTA---GACCCAGAGCCCTTT 572
QY 160 AspGlnIleuSerProPheAlaGlnIleuIleuAspAspGlyArgGlnAlaSerProTy 179
Db 573 GACCAAGGACAGCCCTTTGCTCCAGAGACTGCTGAGACACGCTCAGCAAGCAGCCCTTAC 632
QY 180 TyTrpCysSerThrTyGlyProGlyValProSerProGlySerSerAspValSerThrAla 199
Db 633 CACCCCGCAGCTGTGCGAGGAGGAGCCCTCCCTGAGCACTGACGTCCACCGCA 692
QY 200 ArgThrAlaThrProGlnIleuSerSerHisAlaSerAspSerGlyGlySerAspValAspLeu 219
Db 693 GGGAGCTGTGCTCTCGAGCTCCCACTCCCACTCCAGACTCCGAGTGAATGACGTGAGCTG 752
QY 220 AspLeuThrIleuSerLeuValPheProArgAspAspPheThrAspTyTrpValGlyGlu 239
Db 753 GATCCCACTGATGAGCAAGCTCTTCCCAAGCATGTGTTTCTGATCTGCAAGAGGGGAT 812
QY 240 ProIleHisGlyIleuValArgGlyValArgProArgIleuSerIleuGlyTrpAsp 259
Db 813 CCCAAGACAGCGGAAAGCGGAAACGAGCGGCGCCGAGAAAGCTGAGCAAAAGTACTGGAC 872
QY 260 CysLeuGlnIleuValSerLeuValHisAlaProArgGlyThrHisValLeuTrpGluPheIle 279
Db 873 TGTCTCAAGGACAGAGAGCAAGCAAGCGCCCAAGAGCAACCACTGTGGAGTTTATC 932
QY 280 ArgAspIleuIleuHisProGluIleuAsnGluGlyIleuMetCysTrpGluAsnArgHis 299
Db 933 CGGAGCATCTTCAATCCACCGGAGCTCAAGAGGCTCATGAAAGTGGAGAAATCGGCAT 992
QY 300 GluGlyValPheIleuPheLeuArgSerGluAlaValAlaGlnIleuTrpGlyGlnVal 319
Db 993 GAGGAGGCTTCAAGTCTGCGCTCGAGAGCTGTGGCCCACTATGGGCGCAAAAGAAA 1052
QY 320 LysAsnSerAsnMetTrpTyTrpGluValSerArgAlaMetArgTyTrpTyTrpValArg 339
Db 1053 AAGAAACAGCAACATGACTTCAAGAAAGCTGAGCGGCGCATGAGTACTACTCAAAACGG 1112
QY 340 GluIleuGluValArgGlyValArgGlyValArgGlyValArgGlyValArgGlyValArg 359
Db 1113 GAGATCTGAGAGCGGAGTGGAGTGGCGGAGCTGCTTCAAAAGTTTGGCAAAACCTCAAGC 1172

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QY 360 GlyTrpIleGluGluGluValGlyGluSerArgAsn 371
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RESULT 2
US-09-570-593-4
; Sequence 4, Application US/09570593
; Patent No. 6566063
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xun, Hong
; APPLICANT: Hartowe, Greg
; TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
; FILE OF INVENTION: CANCER
; FILE REFERENCE: 2300-1556
; CURRENT APPLICATION NUMBER: US/09/570,593
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1211)
; OTHER INFORMATION: Human epithelial-restricted with serine box (ESX)
; US-09-570-593-4

Alignment Scores:
Pred. No.: 6,79e-177 Length: 1907
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conservative: 22
Beet Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
DB: Gaps: 2

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QY 21 SerGluAspProThrIleuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
Db 156 TCGGAGAGACTCCACCTGGCTCTGTTTCCCTCTCTCCACCTTTGGGCGGAGACTTG 215
QY 40 ValIeuThrIleuAsnAngInglMetThrIleuGluGlyProGluValAspSerTrpThr 59
Db 216 GTACTGACCTTGAGCAACCCCAATGTCAATTGAGGAGTACAGAGAGGCGGAGCTGGT 275
QY 60 SerGluArgProGlnPheTrpSerLeuThrGlnValIleuGluTrpIleSerTyGlnVal 79
Db 276 GGGGAGACAGCCCGAGTCTGGTTCAGAGCGAGGTTCTGAGCTGATCAGTACCAAGTG 335
QY 80 GluIleAsnIleTyTrpAspAlaSerSerIleAspPheSerArgCysAsnMetAspGlyVal 99
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QY 100 ThrIleuCysSerCysAlaIleuGluGluIleuArgLeuValPheGlyProIleuGluAspGln 119
Db 396 ACCCTCTGCATTTGTGCTTGGAGAGCTGCTGCTGCTTGGGCTCTGGGAGACCAA 455
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Db 456 CTCATGCTCCAGCTGCGAGACCTCACTTCAGCTCTTCTGATGAGTCACTGATGATCAT 515
QY 140 GluIleuIleuGluValAspGlyMetSerPheGlnIleuSerLeuGluValAspLeuGlyProPhe 159
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Qy 160 AspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyr 179
Db 573 GACCAGGAGGAGCCCTTTCGCCAGAGCTGTGACACACGTCAGCAAGCAGCCCTTAC 632
Qy 180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199
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Qy 200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeu 219
Db 693 GGAAGCTGTCCTCTCGAGACTCCCACTCTCAAGCTCCGTCGAACTGACGTGACCTG 752
Qy 220 AspLeuThrGluSerLeuValPheProArgAspAspPheThrAspTyrLeuGlyGlu 239
Db 753 GATCCCACTATGAGCAAGCTCTTCCCAAGATGCTTTGTCATCTCCAAAGAGGGGAT 812
Qy 240 ProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTyrTrpAsp 259
Db 813 CCAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 872
Qy 260 CysLeuGluGlyLysLysSerLysHisAlaProArgLysThrHisLeuTyrGluPheIle 279
Db 873 TGTCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 932
Qy 280 ArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHis 299
Db 933 GGGAGACATCTCATCCACCGAGACTCAAGAGGAGCTCATAGAGTGAGAGATCGCAT 992
Qy 300 GluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTyrGlyGlnLys 319
Db 993 GAAAGGCTCTTCAAGTTCTCGGCTCGAGGCTGTGCTCCCACTATGGGGCCAAAGAAA 1052
Qy 320 LysAsnSerAsnMetThrTyrGlyLysLeuSerArgAlaMetArgTyrTyrLysArg 339
Db 1053 AAGAACGACAACTGACCTACGAGAACTGAGCGGCGCATGAGTCTCTCAAAACGG 1112
Qy 340 GlnIleLeuGlnLysArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSer 359
Db 1113 GAGATCTGGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1172
Qy 360 GlyTyrPheGluGluGluValGlyGluSerArgAsn 371
Db 1173 GGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1208

RESULT 3
US-08-746-789A-1
; Sequence 1, Application US/08746789A
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismail Kola, Martin J. Tyms, Christine DeBuck
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ERF3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1559
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746, 789A
; FILING DATE: No. 5789200ember 15, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

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; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG 50024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5219
; TELEFAX: 610 270 4026
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
; US-08-746-789A-1

Alignment Scores:
Pred. No.: 6,86e-177 Length: 1920
Score: 1712.00 Matches: 323
Percent Similarity: 92.74% Conservative: 22
Best Local Similarity: 86.83% Mismatches: 25
Query Match: 86.25% Indels: 2
DB: 1 Gaps: 2

US-08-978-217-16 (1-371) x US-08-746-789A-1 (1-1920)
Qy 1 MetAlaAlaThrCysGlnLysSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
Db 115 ATGGCTGCAACCTGTAGATTACCAATTTTACGACTCTTCACTGATGATGATGATGATGAT 174
Qy 21 SerGluAspProThrLeuAlaProAlaProPro--ThrThrPheGlyThrGluAspLeu 39
Db 175 TCGAAGAGCTCCACCTTGGGCTCTGTTCCCTCGTGCACCTTGGGGCCGATGACTTG 234
Qy 40 ValLeuThrLeuAsnGlnGlnMetThrLeuGluGlyProGluLysAlaSerTrpThr 59
Db 235 GTACTAGACCTTGACCAACCCCGAGTGTGATGAGGATGACAGAGAGGATGAGGATG 294
Qy 60 SerGluArgProGlnPheThrSerLysTrpGlnValLeuGlnTyrLysSerTyrGlnVal 79
Db 295 GGGAAACAGCCCGAGTTCTGTGTCGAAAGCAGAGCTTCTGACTGATCAGCTACCAAGTG 354
Qy 80 GluLysAsnLysTyrAspAlaSerSerLysPheSerArgCysAsnMetAspGlyAla 99
Db 355 GAGAAAGACAGTACAGACCAAGCCGATTTGACTTCTCAAGATGATGATGATGATGATG 414
Qy 100 ThrLeuCysSerCysAlaLeuGluGluLeuValPheGlyProLeuGlyAspGln 119
Db 415 ACCCTCGCAATTGTGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474
Qy 120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerAspGluLeuSerTrpIle 139
Db 475 CTCATGCTCCAGCTGGAAGACCTCACTTCCAGCTCTTGATGAGCTCAGTTGATGAT 534
Qy 140 GluLeuLeuGlnLysAspGlyMetSerPheGlnGluSerLeuGlyLysPheGlyProPhe 159
Db 535 GAGCTCTGGAAGAGATGAGATGCTTCCAGAGGCCCTA--GACCAGGAGCCCTTT 591
Qy 160 AspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyr 179
Db 592 GACCAAGGAGGAGCCCTTGGCCGAGGAGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAG 651
Qy 180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199
Db 652 CACCCCGCAGCTGTGTCGAGAGGAGCCCTCCCTCCGAGCTGTGACGTCTCCACCGCA 711
Qy 200 ArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeu 219
Db 712 GGAAGCTGTCCTCTCGAGCTCCCACTCTCAAGATCCGTCGAGAGTACGTCGAGCTG 771
Qy 220 AspLeuThrGluSerLysValPheProArgAspAspPheThrAspTyrLysLysGlyGlu 239
Db 772 GATCCCACTGATGAGCAAGCTTCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 831

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QY 240 ProlyshHsGlyValArgGlyValArgProArgGlyLeuSerGlyValTTPASP 259
DB 832 CCCAAGACGCGAAGCGGAAACGAGCGCGGCCCGGAAAGCTGAGCAAAAGAGTACTGGGAC 891
QY 260 CylLeuGluGlyValSerGlySerGlyHsAlaProArgGlyThrHisLeuTTPGluPheIle 279
DB 892 TGCTCGAGGACGAGAAAGACGACGACGCCCGAGAGCACCCACTGTGTGGAGTTATC 951
QY 280 ArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetGlySTPGLuAsnArgHis 299
DB 952 CGGAGACTCTCTCAACCGGAGACTCAAGAGGCGCTCATGAGTGGAGATCCGCAT 1011
QY 300 GluGlyValPheGlyPheLeuArgSerGluAlaValaGlnLeuTTPGlyGlnGlyVal 319
DB 1012 GAAGGCGCTTCAAGTCTCTGCGCTCGAGGCTGTGGCCCAACTATGGGGCAAAAGAAA 1071
QY 320 LysAsnSerMetThrTyrGluValLeuSerArgLamEtArgTyrTyrTyrValArg 339
DB 1072 AAGAACGCAACAGACTACGAGAACCTGAGCGGCGCATGAGATCTACTACMAACGG 1131
QY 340 GluIleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSer 359
DB 1132 GAGATCTCGAAGCGGATGCGATGCGCGGACTGCTTACAAAGTTTGGCAAAACTCAAGC 1191
QY 360 GlyTTPGlyGluGluGluValGlyGluSerArgAsn 371
DB 1192 GGCTGGAAGAGAGAGAGTTCTTCAGATCGGAAAC 1227

RESULT 4
US-09-389-681-282
; Sequence 282, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-389-681-282

Alignment Scores:
Pred. No.: 1,63e-78 Length: 502
Score: 803.00 Matches: 149
Percent Similarity: 93.33% Conservative: 5
Best Local Similarity: 90.30% Mismatches: 11
Query Match: 40.45% Indels: 0
DB: 4 Gaps: 0

US-08-978-217-16 (1-371) x US-09-389-681-282 (1-502)
QY 185 GlyProGlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro 204
DB 6 GGGCGAGGAGAGCCCTCCCGGAGCTCTGACGCTTCCACCGCAGGAGACTGGTGCTTCT 65
QY 205 GlnSerSerHisAlaSerAspSerGlyGlySerSerValAspLeuAspLeuThrGlnSer 224
DB 66 CGGAGCTCCCACTCTCAAGACTCCGGTGAAGTACCTGAGCTCGATCCCATCTGAGTGGC 125
QY 225 LysValPheProArgAspAspPheThrAspTyrLysGlyGluProLysHisGlyLys 244
DB 126 AAGCTCTTCCCAAGCATGTGTTTCGATCGCAAGAGAGGGGATCCCAAGCAGCGGAG 185
QY 245 ArgLysArgGlyArgProArgLysLeuSerGlyValTyrTTPAspCysLeuGluGlyLys 264
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DB 186 CGGAAACGAGCGCGCGCCGAAAGCTGAGCAAAAGACTGTGGACTGTCTCGAGGCGAAG 245
QY 265 LysSerSerHisAlaProArgGlyThrHisLeuTTPGluPheIleArgAspIleLeuIle 284
DB 246 AAGAGCAGACGCGCGCCAGAGGACCCACTGTGTGGATTCATCCGGACATCTCCATC 305
QY 285 HisProGluLeuAsnGluGlyLeuMetGlySTPGLuAsnArgHisGluGlyValPheLys 304
DB 306 CACCCGAGCTCAACAGAGGCGCTCATGAGTGGAGAAATCGGCATGAAAGCGCTTCAAG 365
QY 305 PheLeuArgSerGluAlaValaGlnLeuTTPGlyGlnGlyValLysLysAsnSerMet 324
DB 366 TTCCTCGCTCCGAGGCTGTGGCCCACTATGGGGCAAAAGAAAGACAGCAACATG 425
QY 325 ThrTyrGluLeuSerArgLamEtArgTyrTyrTyrTyrValArgGluIleLeuGluArg 344
DB 426 ACCTACGAGAGAGCTGAGCGGCGCATGAGTACTACTACMAACGGAGATCTCGAAGCG 485
QY 345 ValAspGlyArgArg 349
DB 486 GTGATGCGCGGCGA 500

RESULT 5
US-09-620-405B-282
; Sequence 282, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hedler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-282

Alignment Scores:
Pred. No.: 1,63e-78 Length: 502
Score: 803.00 Matches: 149
Percent Similarity: 93.33% Conservative: 5
Best Local Similarity: 90.30% Mismatches: 11
Query Match: 40.45% Indels: 0
DB: 4 Gaps: 0

US-08-978-217-16 (1-371) x US-09-620-405B-282 (1-502)
QY 185 GlyProGlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro 204
DB 6 GGGCGAGGAGAGCCCTCCCGGAGCTCTGACGCTTCCACCGCAGGAGACTGGTGCTTCT 65
QY 205 GlnSerSerHisAlaSerAspSerGlyGlySerSerValAspLeuAspLeuThrGlnSer 224
DB 66 CGGAGCTCCCACTCTCAAGACTCCGGTGAAGTACCTGAGCTCGATCCCATCTGATGCGC 125
QY 225 LysValPheProArgAspAspPheThrAspTyrLysGlyGluProLysHisGlyLys 244
DB 126 AAGCTCTTCCCAAGCATGTGTTTCGATCGCAAGAGAGGGGATCCCAAGCAGCGGAG 185
QY 245 ArgLysArgGlyArgProArgLysLeuSerGlyValTyrTTPAspCysLeuGluGlyLys 264
DB 186 CGGAAACGAGCGCGCGCCGAAAGCTGAGCAAAAGACTGTGGACTGTCTCGAGGCGAAG 245
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QY 265 LysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgPheIleLeu 284
DB 246 AAGAGCAAGACCGCCGACAGGACCCACCTGTGGAGTTCAATCCGGACATCTTCATC 305
QY 285 HisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGlyValPheLys 304
DB 306 CACCCGAGCTCAACGAGGGGCTCATGAAAGTGGAAGATCGGCATGAAAGCGCTTCAAG 365
QY 305 PheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnIleLysLysAsnSerAsnMet 324
DB 366 TTCCTGGCTCCGAGGCTGTGGCCCACTATGAGGCAAAAGAAAGAACAGCAACATG 425
QY 325 ThrTrpGluLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGluIleLeuGluArg 344
DB 426 ACCTACGAGAAGCTGAGCCGGCCCATGAGTACTACTACAAACGGAGATCTCGAAGCG 485
QY 345 ValAspGlyArgArg 349
DB 486 GTGATGCGCGGCGA 500

RESULT 6
US-09-339-338-282
; Sequence 282, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-282

Alignment Scores:
Pred. No.: 1,63e-78 Length: 502
Score: 803.00 Matches: 149
Percent Similarity: 93.33% Conservative: 5
Best Local Similarity: 90.30% Mismatches: 11
Query Match: 40.45% Indels: 0
Gaps: 0

US-08-978-217-16 (1-371) x US-09-339-338-282 (1-502)
QY 185 GLYProGlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro 204
DB 6 GGGCGAGAGACCCCTCCCTCCCGGAGCTCGACGTCCACCGCAGGAGACTGGTGCTTCT 65
QY 205 GlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSer 224
DB 66 CGAGAGCTCCACCTCCAGACTCGGTGGAAGTGAAGTGAAGTCCGATCCACCTGATGCC 125
QY 225 LysValPheProArgAspAspPheThrAspTyrLysLysGluPheProLysHisGlyLys 244
DB 126 AAGCTCTTCCCGACGATGTTTCGTGACTGCAAGAAAGGGGATCCCAAGCAGCGAAG 185
QY 245 ArgLysArgGlyArgProArgLysLeuSerLysGluTyrTrpAspCysLeuGluGlyLys 264
DB 186 CGGAAACGAGGCGCGCCCGAAGAGTGAAGAAAGTGAAGAGTGTCTCGAGGGCAAG 245
QY 265 LysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgPheIleLeu 284
DB 246 AAGAGCAAGACCGCCGACAGGACCCACCTGTGGAGTTCAATCCGGACATCTTCATC 305
QY 285 HisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGlyValPheLys 304
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DB 306 CACCCGAGCTCAACGAGGGGCTCATGAGTGGAGAAATCGGCATGAAAGCGCTTCAAG 365
QY 305 PheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnIleLysLysAsnSerAsnMet 324
DB 366 TTCCTGGCTCCGAGGCTGTGGCCCACTATGAGGCAAAAGAAAGAACAGCAACATG 425
QY 325 ThrTrpGluLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGluIleLeuGluArg 344
DB 426 ACCTACGAGAAGCTGAGCCGGCCCATGAGTACTACTACAAACGGAGATCTCGAAGCG 485
QY 345 ValAspGlyArgArg 349
DB 486 GTGATGCGCGGCGA 500

RESULT 7
US-09-433-826B-282
; Sequence 282, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-282

Alignment Scores:
Pred. No.: 1,63e-78 Length: 502
Score: 803.00 Matches: 149
Percent Similarity: 93.33% Conservative: 5
Best Local Similarity: 90.30% Mismatches: 11
Query Match: 40.45% Indels: 0
Gaps: 0

US-08-978-217-16 (1-371) x US-09-433-826B-282 (1-502)
QY 185 GLYProGlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro 204
DB 6 GGGCGAGAGACCCCTCCCTCCCGGAGCTCGACGTCCACCGCAGGAGACTGGTGCTTCT 65
QY 205 GlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSer 224
DB 66 CGAGAGCTCCACCTCCAGACTCGGTGGAAGTGAAGTGAAGTCCGATCCACCTGATGCC 125
QY 225 LysValPheProArgAspAspPheThrAspTyrLysLysGluPheProLysHisGlyLys 244
DB 126 AAGCTCTTCCCGACGATGTTTCGTGACTGCAAGAAAGGGGATCCCAAGCAGCGAAG 185
QY 245 ArgLysArgGlyArgProArgLysLeuSerLysGluTyrTrpAspCysLeuGluGlyLys 264
DB 186 CGGAAACGAGGCGCGCCCGAAGAGTGAAGAAAGTGAAGAGTGTCTCGAGGGCAAG 245
QY 265 LysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgPheIleLeu 284
DB 246 AAGAGCAAGACCGCCGACAGGACCCACCTGTGGAGTTCAATCCGGACATCTTCATC 305
QY 285 HisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGlyValPheLys 304
DB 306 CACCCGAGCTCAACGAGGGGCTCATGAAAGTGGAAGATCGGCATGAAAGCGCTTCAAG 365
QY 305 PheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnIleLysLysAsnSerAsnMet 324
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Db      366 TTCTCGGCTCCAGGCTGTGGCCCACTATGGGCCCAAAAAGAAAGAACACACACATG 425
Qy      325 ThTYrGluLylSeuSerArgAlaMeArGTYrTYrTYrLysArgGluLileuGluArg 344
Db      426 ACCTACGAGAGAGCTGAGCCGGCCGACATGAGTACTACTACAAACGGAGATCTCTGAAACGG 485
Qy      345 ValAspGlyArgArg 349
Db      486 GTGATGGCCGGCGA 500

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RESULT 8

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US-09-604-287A-282
; Sequence 282, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-282

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Alignment Scores:
Pred. No.: 1.63e-78 Length: 502
Score: 803.00 Matches: 149
Percent Similarity: 93.33% Conservative: 5
Best Local Similarity: 90.30% Mismatches: 11
Query Match: 40.45% Indels: 0
Gaps: 0

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US-08-978-217-16 (1-371) x US-09-604-287A-282 (1-502)
Qy      185 GlyProGlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro 204
Db      6 GGGCGAGAGAGCCCTCTCCCGGCACTCTGACGTCTCCACCGCAGGAGATGGTCTCT 65
Qy      205 GlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSer 224
Db      66 CGAGAGCTCCCACTCCAGACTCCGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
Qy      225 LysValPheProArgAspAspPheThrAspTYrLysLysGlyLupPolySHISGlyLys 244
Db      126 AAGCTCTTCTCCCGCAGATGTTTCTGACTGCAAGAGGGGAGATCCCAAGCAGGGAG 185
Qy      245 ArgLysArgGlyArgProArgLysLeuSerLysGlyTYrTrpAspCysLeuGluGlyLys 264
Db      186 CGGAAACGAGAGCCGGCCCGCAAGCTGAGCAAGAGAGTGGAGTGTCTCCAGGGCAG 245
Qy      265 LysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeuIle 284
Db      246 AAGAGCAAGACCGCCCGCAGAGGACACCACTGTGGAGATTATCCGGGACATCTCATC 305
Qy      285 HisProGluLeuAsnGluLysLeuMetLysTrpGluAsnArgHisGluGlyValPheLys 304
Db      306 CACCCGAGACTCAACGAGGGCTCTCATGAATGGAGATGGCATGAAAGCGCTTCAAG 365
Qy      305 PheLeuArgSerGlnAlaValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMet 324
Db      366 TTCTCGGCTCCAGAGCTGTGGCCCACTATGGGGCCAAAGAAAGAAAGAACACACATG 425

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Qy      325 ThTYrGluLylSeuSerArgAlaMeArGTYrTYrTYrLysArgGluLileuGluArg 344
Db      426 ACCTACGAGAGAGCTGAGCCGGCCGACATGAGTACTACTACAAACGGAGATCTCTGAAACGG 485
Qy      345 ValAspGlyArgArg 349
Db      486 GTGATGGCCGGCGA 500

```

RESULT 9

```

US-09-834-759-282
; Sequence 282, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-282

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Alignment Scores:
Pred. No.: 1.63e-78 Length: 502
Score: 803.00 Matches: 149
Percent Similarity: 93.33% Conservative: 5
Best Local Similarity: 90.30% Mismatches: 11
Query Match: 40.45% Indels: 0
Gaps: 0

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US-08-978-217-16 (1-371) x US-09-834-759-282 (1-502)
Qy      185 GlyProGlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrPro 204
Db      6 GGGCGAGAGAGCCCTCTCCCGGCACTCTGACGTCTCCACCGCAGGAGATGGTCTCT 65
Qy      205 GlnSerSerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSer 224
Db      66 CGAGAGCTCCCACTCCAGACTCCGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
Qy      225 LysValPheProArgAspAspPheThrAspTYrLysLysGlyLupPolySHISGlyLys 244
Db      126 AAGCTCTTCTCCCGCAGATGTTTCTGACTGCAAGAGGGGAGATCCCAAGCAGGGAG 185
Qy      245 ArgLysArgGlyArgProArgLysLeuSerLysGlyTYrTrpAspCysLeuGluGlyLys 264
Db      186 CGGAAACGAGAGCCGGCCCGCAAGCTGAGCAAGAGAGTGGAGTGTCTCCAGGGCAG 245
Qy      265 LysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeuIle 284
Db      246 AAGAGCAAGACCGCCCGCAGAGGACACCACTGTGGAGATTATCCGGGACATCTCATC 305
Qy      285 HisProGluLeuAsnGluLysLeuMetLysTrpGluAsnArgHisGluGlyValPheLys 304
Db      306 CACCCGAGACTCAACGAGGGCTCTCATGAATGGAGATGGCATGAAAGCGCTTCAAG 365
Qy      305 PheLeuArgSerGlnAlaValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMet 324
Db      366 TTCTCGGCTCCAGAGCTGTGGCCCACTATGGGGCCAAAGAAAGAAAGAACACACATG 425
Qy      325 ThTYrGluLylSeuSerArgAlaMeArGTYrTYrTYrLysArgGluLileuGluArg 344

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[illegible]

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Db          486 GTGATGCCGCACA 500

RESULT 11
US-09-009-913-2
; Sequence 2, Application US/0900913
; Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: Axy's Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
City: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5427 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-009-913-2

Alignment Scores:
Pred. No.:      3,34e-53        Length:    5427
Score:         586.00           Matches:   141
Percent Similarity: 50.26%       Conservative: 51
Best Local Similarity: 36.91%     Mismatches: 86
Query Match:    29.52%           Indels:   104
DB:             3              Gaps:     11

US-08-978-217-16 (1-371) x US-09-009-913-2 (1-5427)
QY      27 AlaProAlaProProThrThr-----PheGlyThrGluAspLeuValLeuThr 42
      ||| ::||::||::||| | | | | | | | | | | | | | | | | | :|
Dd      84 GCtgcctccctcCATCAACAGCACACAGCTATTGGATTTCACCACCGAATCTTAGTA--- 140
QY      43 LeuaSnaBmgInglImetHthrleugluyL--
      |||::| | | | | | | | | | | | | | | | | | | | | | |
Dd      141 -----AAAGAgtCATGTGAATTCGAGAgaAgGTGTGTAATAATTCACACCCGGCAAC 194
QY      53 -----ProgLuYuSaIasErTrphrSerGu----- 61
Dd      195 AACCTCTTACACAGCCGCGACgctGACAGAcACTCTCACAGTGCAATGTTCCAGT 255
QY      62 -----ArgPrGlnPherTpserLyThrGlnVal 71
Dd      255 GGgTTTTTGAAGGCAAGTGGAATAATTATCTCTCAgTACTGGAACCAAGTACCAAGTG 314
QY      72 leuGlutRpIlesErTyrgInVaIgIuYaenUyTYrrApalaserSerlleapPhe 91

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Db      315 TGGAGAGGCTGACGACCTCTGGACACCAAGTCGATGCAATTGTATCTCTTC
Qy      92 SerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluLeuArgLeu
Db      375 CAAGAGTTCACATCAACGGCGAGACCTCTGCGACATGAGTTTGCAGAGTTCAACCCG
Qy      112 ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgLeuThrSerAsn
Db      435 GCGGACGAGGACGGCGGAGCTCTCTACAGCAATTGACGATTCGAAGTGGAAACGCG
Qy      131 -----SerSerAspGlyLeuSerTrpIleIleGluLeuGluGlyAspGlyMetSer
Db      495 CAGTCAGTGTAGTAC-----CTG
Qy      149 PheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGlu
Db      513 TTCACATCCACACACATGCTATGTCACAAAGTGAACAACTGAGCT-----TCC
Qy      169 LeuLeuAspAspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAla
Db      564 ATCATGAACACCTGGAAGACGAGAACTATTATATGACCAACTATGCT-----
Qy      189 ProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSerSerHis
Db      615 -----AGCACA-----
Qy      209 AlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSerTyrValPhePro
Db      621 -----GTAGATTGTTGGACACACAAACTTTCTGC
Qy      229 ArgAspAspPhe-----ThrAspTyrLysLysGlyGluProLysHisGly
Db      651 CCGGCTCAGATCTCCATGACACCAACCACTCTCTCTGTCAGAGTCACTGATATG
Qy      244 LysArgLysArgGlyArgProArgLysLeuSerLysGluTyrTrpAspCysLeuGluGly
Db      711 AAAAAGGAGAAAGACCCCTGCGCAAGTGCACCA-----
Qy      264 LysLysSerLysHisAlaProArgGlyThrHisLeuTyrGluPheIleArgAspIleLeu
Db      750 -----AAGCAACACCCGAGAGGAGCTCATTTAGGAAATTCATCCCGACATCTC
Qy      284 IHisPheGluLeuAsnGluGlyLeuMetLysTrpLysAsnArgHisGluGlyValPhe
Db      801 TTAAACCCACAGAACCAAGATTAATAATGGAGAGCCGATCTGAGCGCTCTTC
Qy      304 LysPheLeuArgSerGlyAlaValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsn
Db      861 AGGTTCTTGAATACAGAGAGTGGCTGCTGCTATGGGGTAAAAAGAAACACACAGC
Qy      324 MetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGlnIleLeuGlu
Db      921 ATGACCATTAATAAAGCTCACCGGCTATGAGAAATTAACAAAGAAATATCTGAG
Qy      344 ArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSerGlyTrpLysGlu
Db      981 CGGTGGATGACGAGAAAGTGTATATAATTGGGAAGATGCCGAGATGGAGAGAA
Qy      364 GluGlu 365
Db      1041 AATGAA 1046

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? STREET: 285 Hamilton Ave, Suite 200
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94301
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/009,913
? FILING DATE: 21-JAN-1998
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Sherwood, Pamela J
? REGISTRATION NUMBER: 36,677
? REFERENCE/DOCKET NUMBER: SEQ-4P
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-327-3231
? TELEFAX: 650-327-3231
?
?
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5510 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? US-09-009-913-3
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? Alignment Scores:
? Pred. No.: 1,54e-52 Length: 5510
? Score: 580.00 Matches: 129
? Percent Similarity: 54.43% Conservative: 43
? Best Local Similarity: 40.82% Mismatches: 78
? Query Match: 29,22% Indels: 66
? DB: 3 Gaps: 7
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? Qy      58 TrpThrSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpIleSerTyr
? Db      356 TGGCAGTAATTCATCTCTGACGATCTGACCAAGTACCAAGTGGAGTGCACACAC
? Qy      78 GlnValGluLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAsp
? Db      416 CTCCTGGACACCAACAGCTGATGCCAATGTATCTCTTCCAGAGTTGCAATCAAC
? Qy      98 GlnAlaThrLeuCysSerCysAlaLeuGluLeuArgLeuValPheGlyProLeuGly
? Db      476 GCGGACACCTCTGCGACATGAGTTTGCAGAGTTCAACCGGCGGACAGGAGCGGG
? Qy      118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsn-----SerSerAspGlu
? Db      536 CAGCTCCTTACAGCAACTTGACGATCTGAAGTGAACGGCCAGTCAGTAGTGAC---
? Qy      135 LeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetSerPheGlnGluSerLeuGly
? Db      593 -----CTGTTCCAGTCCACACCAAT 613
? Qy      155 AspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArg
? Db      614 GTCATTTGCAAGCTGAACAACTGAGCT-----TTCATCTGAACACCTGGAAA
? Qy      175 GlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSer
? Db      665 GACGAGAACTATTATATGACCAACCACTATGCT-----
? Qy      195 AspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGly

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Db 698 -----AGCACA-----703
Qy 215 SerAspValAspLeuAspLeuThrGluSerLeuValPheProArgAspPhe-----232
Db 704 -----GTAGATTGTTGGACAGCAAACTTTGCGGGGCTCAGATCTCCATG 751
Qy 233 -----ThrsAspTyrLysGluProLysHisGlyLysArgGlyArg 249
Db 752 ACAACACACGACTACTCTCTGTTGACAGTCACTGATATGAAAAAGACAAACCCC 811
Qy 250 ProArgLysLeuSerLysGluTyrTrpAspCysLeuGluLysLysSerHisAla 269
Db 812 CTGCGCAAGTCCACACCAAA-----AGCACAAC 841
Qy 270 ProArgGlyThrHisLeuTrpGluPheLeuArgAspLeuLeuHisProGluLeuAsn 289
Db 842 CCGAGAGGAGCTACTATGGGAATTCATCCGACATCTTGAACCCAGACAAAGAAC 901
Qy 290 GluGlyLeuMetLysTrpGluAsnArgHisGluGlyValPheLysPheLeuArgSerGlu 309
Db 902 CCAAGATTAAATAATGGGAAGACCGATCTGAGGGCGCTTTCAGGTTCTTGAATCAGAG 961
Qy 310 AlaValAlaGlnLeuTrpGlyGlnLysLysAsnSerAsnMetThrTyrGluLysLeu 329
Db 962 GCAGTGCTCAGCTATGGGTTAAAAAGAAACACACGACGACATGACCTATGAAAAGCTC 1021
Qy 330 SerArgAlaMetArgTyrTyrTyrLysArgGluLysLeuArgValAspGlyArgArg 349
Db 1022 AGCCGAGCTATGAGATTTACTACAAAGAAATACTGAGCGGTGGATGACGAAGA 1081
Qy 350 LeuValTyrLysPheGlyLysAsnSerSerGlyTrpLysGluGluGlu 365
Db 1082 CTGTATATATAATTGGGAAGAAATGCCGAGGATGAGAGAAATATGA 1129

RESULT 13
US-09-009-913-4
; Sequence 4, Application US/0909913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axy's Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009, 913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5667 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-009-913-4

Alignment Scores:
Pred. No.: 1,61e-52 Length: 5667
Score: 580.00 Matches: 129
Percent Similarity: 54.438 Conservative: 43
Best Local Similarity: 40.828 Mismatches: 78
Query Match: 29.224 Indels: 66
DB: 3 Gaps: 7

US-08-978-217-16 (1-371) x US-09-009-913-4 (1-5667)
Qy 58 TrpThrSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpLysSerTyr 77
Db 513 TGGCATGAATTCATCTCAGTACGTGACCAAGTACCAAGTGTGGAGTGTCTCCAGCAC 572
Qy 78 GlnValGluLysAsnLysTyrAspAlaSerSerLysAspPheSerArgCysAsnMetAsp 97
Db 573 CTCCTGACACCAACCAAGCTGATGCCAATTGTATCTCTTCCAGAGTTTGCACATCAAC 632
Qy 98 GlnValAlaThrLeuCysSerCysAlaLeuGluGluLeuValPheGlyProLeuGly 117
Db 633 GCGAGACCTCTTGCACATGAGTTTGCAGAGTTCAACCCGGCGGACAGGAGCGCGG 692
Qy 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsn-----SerSerAspGlu 134
Db 693 CAGCTCTCTACAGCAACTTGCAGCATCTGAAGTGGAACGCGCAGTGCAGTAGTGAC--- 749
Qy 135 LeuSerTrpLysLeuLeuLeuGluLysAspGlyMetSerPheGlnLysSerLeuGly 154
Db 750 -----CTGTTCCAGTCCACACCAAT 770
Qy 155 AspLeuGlyProPheAspGlnGlySerProPheAlaGlnLysLeuAspAspGlyArg 174
Db 771 GTCATTTGTCAAGCTAACAAGTACAGCT-----TTCATCTGAACACCTGGAAA 821
Qy 175 GlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSer 194
Db 822 GACGAGACATATTATATGACCAACACTATGGT-----854
Qy 195 AspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGly 214
Db 855 -----AGCACA-----860
Qy 215 SerAspValAspLeuAspLeuThrGluSerLysValPheProArgAspPhe-----232
Db 861 -----GTAGATTGTTGGACAGCAAACTTTTCCGGGCTCAGATCTCCATG 908
Qy 233 -----ThrsAspTyrLysGluProLysHisGlyLysArgGlyArg 249
Db 909 ACAACACACGACTACTCTCTGTTGACAGTCACTGATATGAAAAAGACAAACCCC 968
Qy 250 ProArgLysLeuSerLysGluTyrTrpAspCysLeuGluLysLysSerHisAla 269
Db 969 CTGCGCAAGTCCACACCAAA-----AGCACAAC 998
Qy 270 ProArgGlyThrHisLeuTrpGluPheLeuArgAspLeuLeuHisProGluLeuAsn 289
Db 999 CCGAGAGGAGCTACTATGGGAATTCATCCGACATCTCTTGAACCCAGACAAAGAAC 1058
Qy 290 GluGlyLeuMetLysTrpGluAsnArgHisGluGlyValPheLysPheLeuArgSerGlu 309
Db 1059 CCAAGATTAAATAATGGGAAGACCGATCTGAGGGCGCTTTCAGGTTCTTGAATCAGAG 1118
Qy 310 AlaValAlaGlnLeuTrpGlyGlnLysLysAsnSerAsnMetThrTyrGluLysLeu 329
Db 1119 GCAGTGCTCAGCTATGGGTTAAAAAGAAACACCAAGCACTGACCTATGAAAAAGCTC 1178
Qy 330 SerArgAlaMetArgTyrTyrTyrLysArgGluLysLeuArgValAspGlyArgArg 349

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Db 1179 AGCCGACCTATGAGATTTACTACAAAGAAATGACTGCTGTGATGACGAAGA 1238
Qy 350 LeuValTyrLysPheGlyLysAsnSerSerGlyTyrLysGluGlu 365
Db 1239 CTGGTATATTAATTTGGAGAAATGCCCGAGATGGAGAAATGAA 1286

RESULT 14
US-09-020-956-44/C
Sequence 44, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, JIANGCHUN
APPLICANT: DILLON, DAVID C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-020-956-44

Alignment Scores:
Pred. No.: 9,266-50 Length: 852
Score: 543.00 Matches: 124
Percent Similarity: 54.28% Conservative: 41
Best Local Similarity: 40.79% Mismatches: 73
Query Match: 27.36% Indels: 66
Gaps: 7

US-08-978-217-16 (1-371) x US-09-020-956-44 (1-852)

Qy 70 GlnValLeuGluTyrLysSerTyrGlnValGluLysAsnLysTyrAspAlaSerSerIle 89
Db 850 CAGGTGGAGGTGGCTCCATCCTCTCGACACCAACGAGCTGGATGCAATTGATC 791
Qy 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuYserSerCysAlaLeuGluLeu 109
Db 790 CTTTCCAGAGTTCCGATCAACGAGGAGACCTTTGCAAGCATGAGTTGCAAGATTG 731
Qy 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuAspAspLeuThrSer 129
Db 730 ACCGGGGCGGACGAGGAGGCGGCGCAGCTCTCTACAGCAACTTGCACTGGAAGTG 671
Qy 130 Asn-----SerSerAspGluLeuSerTyrLysLeuLeuGluLysAspGly 146

Db 670 AAGGGCAGTGCAGTATGATGAC----- 650
Qy 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166
Db 649 ---CTGTTCCAGTCCACACACAAATGCTATTTGTAACAGTCGAACAACTGAGCTT--- 599
Qy 167 GlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyPro 186
Db 598 ---TCCATCATGAACACCTGGAAGACNMAGAACTATTTATATGACCAACATATGTT--- 545
Qy 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206
Db 544 -----AGCACA----- 539
Qy 207 SerHisAspSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSerLysVal 226
Db 538 -----CTAGATTGTTGGACAGCAAACT 515
Qy 227 PheProArgAspAspPhe-----ThrAspTyrLysGlyGluProLys 241
Db 514 TTCTGCCGGGCTCAGATCTCCATGACCAACCAACCACTTCTGTCAGAGTCACCT 455
Qy 242 HisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluTyrTrpAspCysLeu 261
Db 454 GATATGAAAAGAGGAGAGACCCCTGCCAGTGCACACCAA----- 410
Qy 262 GluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrPgluPheLeuAsp 281
Db 409 -----AAGCACAACCCGAGAGGAGCTCATTTAGGAATTCATCCCGCAG 365
Qy 282 IleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTyrPgluAsnArgHisGluGly 301
Db 364 ATCCTCTGAACCCCAACAAACCCAGATTATTAATGGGAACGAGATCTGAGGCG 305
Qy 302 ValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTyrGluLysLysLysAsn 321
Db 304 GTCTTCAAGTCTTGAATTCAGAGGAGTGGCTCAGCTATGGGGTAAAGAAAGAACAC 245
Qy 322 SerAspMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGluIle 341
Db 244 AGCAGCATGACCTATTAATAAAGCTCAGCCGAGCTATGATATTAACAAAGAAATTT 185
Qy 342 LeuGluArgValAspGlyArgLeuValTyrLysPheGlyLysAsnSerSerGlyTyr 361
Db 184 CTGAGCGTGTGGATGAGAGAGACTGTATTAATTTGGAAAGAAATCCCGAGGATGG 125
Qy 362 LysGluGluGlu 365
Db 124 AGAGAAATGAA 113

RESULT 15
US-09-030-607-44/C
Sequence 44, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, JIANGCHUN
APPLICANT: DILLON, DAVID C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/030,607
 FILING DATE: 25-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 852 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-030-607-44

Alignment Scores:
 Pred. No.: 9.26e-50 Length: 852
 Score: 543.00 Matches: 124
 Percent Similarity: 54.28% Conservative: 41
 Best Local Similarity: 40.79% Mismatches: 73
 Query Match: 27.36% Indels: 66
 DB: 3 Gaps: 7

US-08-978-217-16 (1-371) x US-09-030-607-44 (1-852)

QY 70 GlnValLeuGluTrpIleSerTyrglnValGluLysAsnLysTyraAspAlaSerSerIle 89
 DB 850 CAGGTGGAGTGGCTCATCTCTGACACCAACGCTGGATGCGCAATTGTATC 791
 QY 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluLeu 109
 DB 790 CTTTCCANAGTTCGACATCAACGGGAGACCTTTGGACGATGAGTTGCGAGAGTTC 731
 QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129
 DB 730 ACCCGGCGGCGACGCGGCGGCGCANCTCTACAGCAACTTGCGACATCTGAAGTGG 671
 QY 130 Asn-----SerSerAspGluLeuSerTrpIleLeuLeuGluLysAspGly 146
 DB 670 AACGGCCAGTGCAGTGTGAC----- 650
 QY 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166
 DB 649 ---CTGTTCCAGTCCACACACATGTGATGTCAAGACTGACAACTGAGCCT----- 599
 QY 167 GlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyrrTyrcysSerThyrglyPro 186
 DB 598 ---TCCATCATGAACCTCGAAAGACNAGAACTATTATATGACACCAACTATAGGT--- 545
 QY 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206
 DB 544 -----AGCACA----- 539
 QY 207 SerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGlnSerLysVal 226
 DB 538 -----CTAGATTGTTGGACAGCAAAACT 515
 QY 227 PheProArgAspAspPhe-----ThrAspTyrrLysLysGlyGluProLys 241
 DB 514 TTCTGCGCGGCTCAGATCTCATGACACCAACCACTTCTCTGTCGAGAGTCACT 455
 QY 242 HisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluTyrrTrpAspCysLeu 261
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 QY 262 GluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAsp 281

DB 409 -----AMGCACAACCCGAGAGGAGCTCACTTATGGGAATTTCATCCGCGAC 365
 QY 282 IleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGly 301
 DB 364 ATCTCTTAACCCAGACAAAGAACCCAGATTAAATTAATGGGAAGACCGAATCTGAGGCG 305
 QY 302 ValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysAsn 321
 DB 304 GTCTTAGAGTTCTTGAATCAAGAGGAGTGGCTAGCTATGGGGTAAAGAAAGAACCAAC 245
 QY 322 SerAsnMetThrTyrgluLysLeuSerArgAlaMetArgTyrrTyrrLysArgGluIle 341
 DB 244 AGCAGCATGACCTATGAAAGCTCAGCCAGCTATGAGTATTACTTACAAAGAGAAATT 185
 QY 342 LeuGluArgValAspGlyArgArgLeuValTyrrLysPheGlyLysAsnSerSerGlyTrp 361
 DB 184 CTGGAGCGTGTGATGAGACGAAGACTGTATATTAATTTGGAAAGATGCCCGAGGATGG 125
 QY 362 LysGluGluGlu 365
 DB 124 AGAGAAAATGAA 113

Search completed: November 15, 2004, 23:13:57
 Job time : 125.561 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:42:48 ; Search time 3635.71 Seconds
(without alignments)
11515.905 Million cell updates/sec

Title: US-08-978-217-15

Perfect score: 7752

Sequence: 1 GGATCCTTCCAGGACACTGA.....CAGAGGGGCTCTGATCC 7752

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCRT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	235.4	3.0	395	16	US-10-152-319A-670 Sequence 670, App
2	216	2.8	1907	14	US-10-097-340-74 Sequence 74, Appl
3	216	2.8	1907	15	US-10-291-808-27 Sequence 27, Appl
4	215.6	2.8	1915	9	US-09-964-824A-101 Sequence 101, App
5	215.6	2.8	1915	9	US-09-964-824A-563 Sequence 563, App
6	215.6	2.8	1915	9	US-09-880-107-3420 Sequence 3420, Ap
7	215.6	2.8	1915	9	US-09-967-768A-192 Sequence 192, App
8	215.6	2.8	1917	9	US-09-922-217-1105 Sequence 1105, Ap
9	215.6	2.8	1917	13	US-10-025-380-1105 Sequence 1105, Ap
10	215.6	2.8	1956	16	US-10-264-049-756 Sequence 756, App
11	215.6	2.8	1996	9	US-09-925-301-207 Sequence 207, App
12	215.6	2.8	2269	15	US-10-131-410-64 Sequence 64, Appl

C 13	185.8	2.4	1435	15	US-10-017-161-1953 Sequence 1953, Ap
C 14	185.8	2.4	1435	15	US-10-293-798-1601 Sequence 1601, A
C 15	179	2.3	229	18	US-10-425-115-58949 Sequence 58949, A
C 16	176.2	2.3	626	9	US-09-922-217-853 Sequence 853, App
C 17	176.2	2.3	626	9	US-09-833-263-853 Sequence 853, App
C 18	176.2	2.3	626	13	US-10-025-380-853 Sequence 853, App
C 19	174.2	2.2	620	14	US-10-060-036-2379 Sequence 2379, Ap
C 20	166	2.1	437	9	US-09-998-598-2216 Sequence 2216, Ap
C 21	163.8	2.1	275	14	US-10-060-036-3361 Sequence 3361, Ap
C 22	163.8	2.1	499	9	US-09-998-598-2280 Sequence 2290, Ap
C 23	163.8	2.1	502	9	US-09-604-287A-282 Sequence 282, App
C 24	163.8	2.1	502	9	US-09-834-759-282 Sequence 282, App
C 25	163.8	2.1	502	9	US-09-339-338-282 Sequence 282, App
C 26	163.8	2.1	502	10	US-09-551-621-282 Sequence 282, App
C 27	163.8	2.1	502	13	US-10-007-805-282 Sequence 282, App
C 28	163.8	2.1	502	14	US-10-076-622-282 Sequence 282, App
C 29	163.8	2.1	502	15	US-10-124-805-282 Sequence 282, App
C 30	148	1.9	451	9	US-09-998-598-32 Sequence 32, Appl
C 31	144	1.9	528	14	US-10-066-543-3333 Sequence 3333, Ap
C 32	140.2	1.8	355	9	US-09-867-701-4818 Sequence 4818, Ap
C 33	132.2	1.7	563	9	US-09-833-263-944 Sequence 944, App
C 34	132.2	1.7	563	9	US-09-833-263-944 Sequence 944, App
C 35	132.2	1.7	563	13	US-10-025-380-944 Sequence 944, App
C 36	126.8	1.6	6191	17	US-10-322-281-645 Sequence 645, App
C 37	125.8	1.6	33488	15	US-10-085-117-235 Sequence 235, App
C 38	125.6	1.6	237	16	US-10-305-720-927 Sequence 927, App
C 39	124.4	1.6	92076	17	US-10-322-281-465 Sequence 465, App
C 40	124.2	1.6	93329	17	US-10-322-281-817 Sequence 817, App
C 41	124	1.6	84410	17	US-10-322-281-817 Sequence 817, App
C 42	124	1.6	84410	17	US-10-322-281-817 Sequence 817, App
C 43	123.8	1.6	65559	9	US-10-087-192-73 Sequence 73, Appl
C 44	123.6	1.6	5973	13	US-10-087-192-73 Sequence 73, Appl
C 45	123.4	1.6	493631	13	US-10-087-192-205 Sequence 205, App

ALIGNMENTS

RESULT 1
US-10-152-319A-670/c
; Sequence 670, Application US/10152219A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Blashoff, Michael
; TITLE OR INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22


```

US-10-291-808-27
; Sequence 27, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-291-808-27

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Query Match	2.8%;	Score 216;	DB 15;	Length 1907;
Best Local Similarity	66.7%;	Pred. No. 4, 3E-54;		
Matches 456;	Conservative 0;	Mismatches 195;	Indels 33;	Gaps 9;
QY	6999	AGGTATTACTACAAACGGAGATCTTGAAACGGGTGATGCGCGAGCGCTGCTTACAAAG	7056	
Db	1095	AGGTACTCTCTCAAAACGGAGATCTTGAAACGGGTGATGCGCGAGCTGCTTACAAAG	1154	
QY	7059	TTTGGCAAGAACTCTAGTGGCTGGGAAGAAAGAGGTGTGAGAGATCGGAATTAAAGA	7118	
Db	1155	TTTGGCAAAACTCAAGCGGCTGGGAAGAAAGAGGTTCCTCAAGTGGAACTGAAGG	1211	
QY	7119	TCGGGGCTGAGCCCAAGACCTGACTCAGAGCATGAATCCAGAACTGAAGCCCTCTGGA	7178	
Db	1215	TTGGAACTATACCCGGGACCAAACTCAGGACCATCGAGGCGCTGCAAACTCTCTGGGA	1274	
QY	7179	GGACAGGAGAGGCTGTACGGCCCCCTTAAACATGATGTGTTCCCTGTGTCTGTAGAAG	7233	
Db	1275	GGACAGGAGAGGCTGATATGAG-CCCCCTCACTGGGGATCTCCCACTGTGCTGTGAAG	1333	
QY	7239	GAAGAACCTGTGGGCGTGCCTCTGC---AGTCTCTCAAGTGCAGCCCTTGGGCTC--	7292	
Db	1334	AAAGCTAGTGTGTGTGTATGTACAGCCATGCTCTTGGACCTGGAGACTATAGGCTTCGC	1392	
QY	7294	--TCTCTCGCCCTCTTGAATTTACAGACCCCGGCTTTGAACCAACTTGT-----	7341	
Db	1394	CTCCCAACCTCTCTTGAATTTACAAACCCCTGGGCTTTGAAGCTGACTTTATAGCTGCA	1453	
QY	7342	--TGGATATCTCTCCACGCTGATCTTCAGTTCCTCCCGTCCCAACTGAGCTGCAAT	7392	
Db	1454	AGGTATCTCTCTTATATCTGTGGGCTCTCTCAAAACCAAGTCTTAGACCTTAATATCAGAC	1511	
QY	7400	GAGAC---CAACCTGACAGATGCTTGCTGCTCAGCCCAAGAGGCTGTGGGAGACTGTGGCAGG	7456	
Db	1514	AAACACTTCTCTCTGACAGCACTTGAATGAGCTGAAGGAGGCTTGGAGAGCCCT---AG	1565	
QY	7457	AGACTGCAAGGACCGAGGGGACAGGGTTGTGTCTCTCGTACTTC---CTGACCTGCTTC	7511	
Db	1570	GGAGACCTGATGTGAGAGAGACAGAGGAGGCTCAGACACTTCTTCTGAGCTGACGTT	1622	
QY	7514	CACCTCTTGGCTCACTACTCAGAGGCTCCACAGACGGGGGTGGATCA-TCCTAATTTATG	7572	
Db	1630	CACCTCCCTGCTCAATGCTGTGGGCTCCAGCGGCAAGGGGTCAAGGACACTCCAAATTTATG	1688	
QY	7573	TGCTATA--AAATTCCAGGTGTATATAGAGCTATTTTTTTCTAAAGCATTTCCCTCC	7633	

Db 1690 TGCATATTAATATGTCAGATGTCATAGAGATCTATTTTCTAAAAACATTCCTCCCTCC 1749

Qy 7631 CTGCTCTTCACACTGAGTGTGG 7654

Db 1750 CACTCCTCTCCCAAGAGTGTGG 1773

RESULT 4
US-09-964-824A-101
Sequence 101, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:
APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964, 824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236, 033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236, 032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236, 028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: PatentIn version 3.0
SEQ ID NO 101
LENGTH: 1915
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-824A-101

Query Match	2.88	Score 215.6	DB 9	Length 1915	
Best Local Similarity	65.68	Pred. No. 5.6e-54			
Matches 449	Conservative 0	Mismatches 204	Indels 31	Gaps 8	
Qy 6999	AGGTATTACTACAAACGGAGATCCTGTGAACGGGTGATGCGACGAGCTGTCTACAG				7058
Db 1119	AGGTACTACTACAAACGGAGATCTGTGAACGGGTGATGCGCGAGCTGTCTACAG				1178
Qy 7059	TTTGGCAAGAACTCTAGTGGCTGGAGAGAAAGGTTGAGAGAGTCCGAAATTAAAG				7118
Db 1179	TTTGGCAAAAACCTCAACGGCTGGAGAGAGAAAGGTTCTCCAGAGTCGAACTGAAGG				1238
Qy 7119	TCGGGCGTCGACCCAGAGACTGACGCAATGAACCTCAAGACTGAAGCTTCCTGGA				7178
Db 1239	TTGGAACTATACCGGGAACMAACTCAAGCACTCGAGGCTGCAAACTTCTCTGGA				1298
Qy 7179	GGAAGGCAAGGCTGACGGCCCCCTTAACATGATGTTCTCTGTGTGCTGTAGAG				7238
Db 1299	GGAAGGCAAGGCTGAGATG - CCGCTTCCAGTGGGAATGCTCCAGCTGTGCTGTAGAG				1355
Qy 7239	GAAAGACCTGTGGGGCGTGCCTCTGC - - AGTCTCTCAAGTGAAGCTTTGGCTC - -				7295
Db 1358	AAGCTGATGTTTGTGTATGTGAGGCATGCTCTGGGACTCGAGACTATGACCTTCG				1417
Qy 7294	--TCTCTCGCCCTCTGGAATTCAAGCCCCGGGTTTGAACCAACTGTTCGA - - - - -				7345
Db 1418	CTCCCAACCCCTCTCTTGGAAATTAACAAGCCTGGGGTTTGAAGCTGACTTATATGCTCA				1477
Qy 7346	-----TAACTTTCAGCTGTGATTTCCAGTTCCCTCCCGCTCCCAATGACCTGCA				7397
Db 1478	AGTGTATCTCTTTATATCTGGTGCCTCTCAAAACCAAGTCTCAAGACTTAATGAGACA				1533
Qy 7398	ATGAGACCCACTTGCAGATGCTTGCGCTCAAGCAAGAGGCTGGGAGACTGTGACAGA				7455
Db 1538	ACACCTTCTCTCTCAAGCACTGGAAGTGAAGCAAGAGGCGCTGGG - GAGGCCCTAGGG				1599
Qy 7458	GACTGCAAGGAGCGAGGGGACAGGGTGTGTCTCGG - - -TACTCTCGGACTGCTTC				7513
Db 1596	GAGCAGCGTGTGAGAGAGACAGAGGAGGAGGCTCCAGACCTTCTTTGTGACTTGCGCTT				1655

Qy	7514	CACCTCTTGTGTCAGTA	CTCAGGGCTCCACA	CGGGGGTGGAATCA--TTCCATAATTATG	7512
Db	1656	CACCTCCCCTGCTCAGTGC	TGTGGGGCTCCA	CGGGCAGGGGTGAGAACACTCCCTAATTATG	1715
Qy	7513	TGC--TATAAATATTTCCAGTGTATATATG	AAGCATTTTTTCTMAAGA	CAATTCGCCCTCC	7610
Db	1716	TGCTATATATAAATATGTCAGATGTACATATG	ATGATATATTTTCTPAAAA	CAATTCCTCC	1775
Qy	7631	CTGCTCTTCTCCACGAGTGC	TGGG	7654	
Db	1776	CACCTCTCTCCACAGAGTGC	TGGG	1799	

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RESULT 5
US-09-964-824A-563
; Sequence 563: Application US/09964822A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 563
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-964-824A-563

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Query Match	2.8*	Score	215.6	DB	9	Length	1915
Best Local Similarity	65.6*	Pred.	No.5.66-54*				
Matches	449	Conservative	0	Mismatches	204	Indels	31
							Gaps
							8
Qy	6999	AGGTATTACTTACCAACCGGAGACTCTTGAAACGGGTGATGCGCCGACGCGCTGCTTCAACG	7058				
Db	1119	AGGTACTACTTCAACCGGAGATCTTGAAACGGGTGATGCGCCGACCTGCTTCAACG	1178				
Qy	7059	TTTGGCAAGACTCTAGTGGCTGGAAGGAAGAAGGTGAGAGAGTCGGAATTAAAGA	7118				
Db	1179	TTTGGCAAACTCAAGCGCTGGAAGGAAGAGGTTCTCCAGAGTCGGAATTGAGG	1238				
Qy	7119	TCGGGGCTGACCCAGACCTGACTCAGGCATGAATTCAGAACTGAAGCCTTCTGAA	7178				
Db	1239	TTGGAACTATATCCGGGACCAACTCAGGACCACTCGAGGCTGCAAACTTCTCTGGGA	1298				
Qy	7179	GGAAGAGAGGCTCGAAGCGCCCTTACAGATATGCTTCCGTGTTGCTGTGAAGAG	7238				
Db	1299	GGAAGAGAGGCTCGAGATG-CCCTTCCATGGGAATATCTCCAGCTGTGTTGGAAG	1357				
Qy	7239	GAAAGACTGTGGGCGTGCCTCTGC--AGTCTCTCAAGTCAGACTTGTGGCTC--	7293				
Db	1358	AAGCTGATGTTTTGTGTATTTGTAGCAGCATGCTCTGGGACTCGGAAGCTATGCGCTCGC	1417				
Qy	7294	--TCTCTCGGCTCTTGGAAATTACAGCCCCGGGTTGAACCAATTGTTCA-----	7345				
Db	1418	CTCCCAACCTCTCTTGGAAATTACAGCCCCGGGTTGAAGCTGACTTTATAGCTGA	1477				
Qy	7346	-----TAAGCTCTTCAAGCTGATTTCAAGTTCCTCCGCTCCCAATGAGCTGCA	7397				
Db	1478	AGTGTATCTCTTTATATGTGATGCTCTTCAACCCAGCTCTCAACACTAATATGCAACA	1537				
Qy	7398	ATGAGACCCACTGTCAGATGCTTGCGCTCAGCCAGAGAGGCTGGAGACTGTGACAGA	7457				
Db	1538	ACACCTTCTCTGTGAGACACTGTGACTGAACCAAGAGGCGCTGG--GAGCGCTGTAGG	1595				

Qy	7458	GACTCGACGGGACCGAGGGGACAGGGGTGTGCTCCGG-----TACTCTGTGGACATCGCTCC	751.3
Db	1596	GAGCACCCTGATGGAGAGACAGACAGCGGGGCTTCAGACACTCTTTCTGTGGACTGGCGTT	1655
Qy	7514	CACCTCTTTGGCTCAGTACTACAGGCTCCACAGACGGGGGTGGATCA--TCCCTTAATTTATG	7572
Db	1656	CACCTCCCTGCTCAGTGTCTTGGGCTTCACACGGGGGACAGGGGTAGAGACACTCCCTAATTTATG	1715
Qy	7573	TGC--TATTAATATTTCCAGGTGTATATAGAGAGCTATTTTTTTCTAAGACATTTCCCTCC	7630
Db	1716	TGCTATATTAATATATGTACAGATGTACATATAGAGATCTATTTTTTTCTAATAACATTTCCCTCCC	1775
Qy	7631	CTGCTCTTTCCACATGAGTGTGG	7654
Db	1776	CACCTCTCTCCACAGAGTCTGG	1799

RESULT 6
 US-09-880-107-3420
 Sequence 3420, Application US/09880107
 Patent No. US20020142981A1
 GENERAL INFORMATION:
 APPLICANT: Horne, Darci T.
 APPLICANT: Vockley, Joseph G.
 APPLICANT: Scherf, Uwe
 APPLICANT: Gene Logic, Inc.
 TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 FILE REFERENCE: 44921-5028-WO
 CURRENT APPLICATION NUMBER: US/09/880,107
 CURRENT FILING DATE: 2001-06-14
 PRIOR APPLICATION NUMBER: US 60/211,379
 PRIOR FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: US 60/237,054
 PRIOR FILING DATE: 2000-10-02
 NUMBER OF SEQ ID NOS: 3950
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3420
 LENGTH: 1915
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843
 US-09-880-107-3420

	Query Match	2.8%;	Score 215.6;	DB 9;	Length 1915;	
	Best Local Similarity	65.6%;	Pred. No. 5.66-54;			
	Matches 449;	Conservative	0;	Mismatches 204;	Indels 31;	Gaps 8;
Oy	AGGATTAATCTCAACAACGGAGATCTCTGAAACGGGTGATGGCCACGAGCTGCTTACAAAG					7058
Db	1119 AGGATCTAATCAACAACGGAGATCTCTGAAACGGGTGATGGCCACGACTGCTTACAAAG					1178
Oy	7059 TTTGGCAAGAACTCTAGTGCGCTGAGAGAGAAAGAGGTTGGAGAGAGTCGAAATTAAAGGA					7118
Db	1179 TTTGGCAAAAACCTCAACCGGCTGAGAAAGAGAAAGAGTTCTTCACAGTCGGAATCGAGGG					1238
Oy	7119 TCGGGGCTGGAACCCAGAACCTGCAAGCTCAAGCATGAATCTCAAGAACTGAAGCCTTCTCGGA					7178
Db	1239 TTGGAACTATACCCGGGACCAAACTCACCGGCACTCGAGGCTCGCAAACTTCTCTGGGA					1298
Oy	7179 GGAAGAGCAGGCTCGAAGGCCCCCTTAACATGATGTGTTCCCTGTGTGCTGTAGAGAG					7238
Db	1299 GGAAGAGCAGGCCACGATATGG-CCCTTCACATGGGGAATGCTCCAGCTGTGTGTGGAGAG					1357
Oy	7239 GAAGAACCTGTTGGGCGTGCCCTCTGC--AGTCTCTCAAGTGCAGCCTTTGGCCTTC--					7293
Db	1358 AAGCTGATGTTTGTGTATGTATGTAGCGCAATGCTCTGGGACTCGGAACATATATGCTCTGCG					1417
Oy	7294 --TCTCTCGGCCCTTGGAATTACAGCCCGGCTTGAACCAACTTGTTCGA-----					7345
Db	1418 CTCCCAACCTCTCTTTGGAATTACAGCCCTGGGGTTTGAAGCTGACTTATATAGCTCA					1477

QY 7346 -----TACTCTTCAGCTGTGATTCAGTTCCCTCCCTCCCAACATGAGCTGCA 7397
DB 1478 AGGTATATCTCTTTATCTGTGTCTCTCTCAAAACAGTCTCAGACACTTAATGACAGCA 1537
QY 7398 ATGAGACCACTGACAGATCTGTGGCTTCAAGCAAGAGGCTGGGAGACTGTGGCAGA 7457
DB 1538 ACACCTTCTCTCCGACAGACACTGTGACTGACCAAGAGGCTGGG--GAGGCTTAGGG 1595
QY 7458 GACTGAGGAGGAGGAGGAGGAGGTTGTCTCGG-----TACTTCTGTGAGCTGCTTC 7513
DB 1596 GACACCGGTATGAGAGAGAGAGAGAGGAGGCTTCACAGACTTCTTCTGTGAGCTGGGCTT 1655
QY 7514 CACTCTTGTCTCAGTACTCAGGCTCCACAGAGGAGGCTGAGATCA-TCCCTAATTATG 7572
DB 1656 CACTCCCTGCTCAGTGTCTGGCTCCAGGAGGAGGCTCAGAGCACTCCCTAATTATG 1715
QY 7573 TGC--TATTAATTTCCAGGTGTATATAGAGACTATTTTCTTAAAGCATTTCCCTCC 7630
DB 1716 TGTATATTAATATATGTCAGATGTACATAGATCTATTTTCTTAAACATTTCCCTCC 1775
QY 7631 CTGCTCTCTCCAGTGTGCTGG 7654
DB 1776 CACTCTCTCCACAGAGTGTGG 1799

RESULT 7

US-09-967-768A-192

Sequence 192, Application US/09967768A
Patent No. US2002015087A1

GENERAL INFORMATION:

APPLICANT: Augustus, Meena

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

FILE REFERENCE: 689290-72

CURRENT APPLICATION NUMBER: US/09/967, 768A

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US/60/236,109

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,111

PRIOR FILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 325

SOFTWARE: PatentIn version 3.0

SEQ ID NO 192

LENGTH: 1915

TYPE: DNA

ORGANISM: Homo sapiens

US-09-967-768A-192

Query Match 2.8%; Score 215.6; DB 9; Length 1915;

Best Local Similarity 65.6%; Pred. No. 5.6e-54;

Matches 449; Conservative 0; Mismatches 204; Indels 31; Gaps 8;

QY 6999 AGGTATTACTACAAACGGAGATCTGGAACGGGTGATGCGGCTGCTCAAG 7058
DB 1119 AGGTACTACTACAAACGGAGATCTGGAACGGGTGATGCGGCTGCTCAAG 1178
QY 7059 TTGGCAAGAACTCTAGTGGCTGGAAGAAAGAGTTGAGAGAGTCCGAATTAAGA 7118
DB 1179 TTGGCAAGAACTCTAGTGGCTGGAAGAAAGAGTTGAGAGAGTCCGAATTAAGA 1238
QY 7119 TCGGGCTGAGCCAGAGACTGACTCAGCATGAATCTCCGAAGTGAAGCTTCTCGAA 7178
DB 1239 TTGGAATATATACCGGAGACCAACTCAGCACTCAGAGCTGCAAACTTCTCGGA 1298
QY 7179 GACAGGAGAGCTGAGAGGCGCCCTTAACATGATGTTCCCTGTTGTTGAGAG 7238
DB 1299 GACAGGAGAGCTGAGAGGCGCCCTTAACATGATGTTCCCTGTTGTTGAGAG 1357
QY 7239 GAGAACTGTTGGGCGTGTCTGCG--AGTCTCTCAAGTGCAGCCTTTGGCTC-- 7293
DB 1358 AAGCTATGTTTGTGTATTTGTCAGCATGTCTCTGAGACTCGAAGACTATATGCGCTCGC 1417

RESULT 8

US-09-922-217-1105

Sequence 1105, Application US/09922217

Patent No. US2002007641A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Lodes, Michael J.

APPLICANT: Secrist, Heather

APPLICANT: Benson, Darin R.

APPLICANT: Weagener, Madeleine Joy

APPLICANT: Stolk, John A.

APPLICANT: Wang, Tonglong

APPLICANT: Jiang, Yudi

APPLICANT: Smith, Carole Lynn

APPLICANT: King, Gordon E.

APPLICANT: Wang, Aljun

APPLICANT: Clapper, Jonathan D.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

FILE REFERENCE: 210121, 471C13

CURRENT APPLICATION NUMBER: US/09/922,217

CURRENT FILING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 1124

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1105

LENGTH: 1917

TYPE: DNA

ORGANISM: Homo sapiens

US-09-922-217-1105

Query Match 2.8%; Score 215.6; DB 9; Length 1917;

Best Local Similarity 65.6%; Pred. No. 5.6e-54;

Matches 449; Conservative 0; Mismatches 204; Indels 31; Gaps 8;

QY 6999 AGGTATTACTACAAACGGAGATCTGGAACGGGTGATGCGGCTGCTCAAG 7058
DB 1121 AGGTACTACTACAAACGGAGATCTGGAACGGGTGATGCGGCTGCTCAAG 1180
QY 7059 TTGGCAAGAACTCTAGTGGCTGGAAGAAAGAGTTGAGAGAGTCCGAATTAAGA 7118
DB 1181 TTGGCAAGAACTCTAGTGGCTGGAAGAAAGAGTTGAGAGAGTCCGAATTAAGA 1240
QY 7119 TCGGGCTGAGCCAGAGACTGACTCAGCATGAATCTCAGAACTGAAGCTTCTCGAA 7178

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Db      1241 TTGGAACTATATACCCGGGACCAAACTCAGGACCACTGAGGCGCTGCAGAACTTCTCGGGA 1300
Qy      7179 GGAAGGACGAGCGCTGACGCGCCCTTAACTGATGTTCCCTGTGTCTGTAGAGAG 7238
Db      1301 GGAAGGACGAGCGCTGACGCGCCCTTAACTGATGTTCCCTGTGTGTAGAGAG 1359
Qy      7239 GAAGAACTGTGGCGCTGCGCTCTGCG---AGTCTCTCAAGTGCAGACCTTGGGCTC-- 7293
Db      1360 AAGCTATGTTTTGTGTATGTATGTACGATGCTGTGGAGCTGGAGACTATGGCTCGC 1419
Qy      7294 --TCTCTGCGCTCTTGGATTAACAAGCCCGGTTTGAACCACTTGTTCGA----- 7345
Db      1420 CTCGCCACCTCTCTTGAATTAACAAGCCCGGTTTGAACCACTTGTTCGA 1479
Qy      7346 -----TAAGTCTTCAAGTGTATTCAGTTCCTCTCCGCTCCCAAGTGCAGCA 7397
Db      1480 AGTGTATCTCTTTTATCTGTGTGCTCTCTCAAACTGCTCAGACACTTAAATGACAGCA 1539
Qy      7398 ATGAGACCACTGACAGATGCTGAGCTCAGCCCAAGAGGCTGGGAGACTGTGGCAGGA 7457
Db      1540 ACACCTTCTCTCTGACAGACACTGAGACTGAGCCAAAGAGGCTGGGG--GAGGCCCTAGGG 1597
Qy      7458 GACTGACGAGGACGAGGAGGACAGAGGTTGTCTCTCG---TACTTCTGAGACTGCTTC 7513
Db      1598 GAGCACCGTATGAGAGAGAGAGAGGAGGAGGCTCCAGACCTTCTTGTGAGCTGGGCTT 1657
Qy      7514 CACCTCTTGTGACGATCAGGCTCAGAGCTCAGACAGCGGGGTGAGATCA--TCCCTAATTATG 7572
Db      1658 CACTCTCCCTGCTCAGAGCTGTGGGCTCCAGCGGAGGGGTGAGAGCACTCCCTAATTATG 1717
Qy      7573 TGC--TATAAATATTCAGAGTGTATATAGAGACTATTTTCTAAGCATTTCCCTCC 7630
Db      1718 TGTATATTAATATATGTCAGATGTACATAGATCTATTTTCTAATAAATCCCTCCC 1777
Qy      7631 CTGCTCTTCTCCACTGAGTCTGG 7654
Db      1778 CACTCTCTCCCAAGAGTCTGG 1801

```

RESULT 9

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US-10-025-380-1105
; Sequence 1105, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Jiang, Yujun
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-1105

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Query Match 2.8%; Score 215.6; DB 13; Length 1917;
 Best Local Similarity 65.6%; Pred. No. 5.6e-54;
 Matches 449; Conservative 0; Mismatches 204; Indels 31; Gaps 8;

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Qy      6999 AGGTATTACTTACCAAGGAGATCTTGGAAACGGGTGTGATGCGGACGCTCTCTACAG 7058
Db      1121 AGGTACTTACTTACCAAGGAGATCTTGGAAACGGGTGTGATGCGGACGCTCTCTACAG 1180
Qy      7059 TTGGCAAGAACTCTAGTGGCTGGAAGAAAGAGAGTGTGAGAGTGTGGAATTAAAGA 7118
Db      1181 TTTGGCAAAACTCAAGCGGCTGGAAGAAAGAGTGTGAGAGTGTGGAATTAAAGA 1240
Qy      7119 TCGGGCTGGAACCCAGACCTGACTGAGCATGAATCCAGAACTGAACTTCTGAA 7178
Db      1241 TTGGAATATTAACCCGGAGCAAACTCAGGACCACTGAGGCTGTGAACTTCTCGGA 1300
Qy      7179 GGAAGGACGAGCTGACGCGCCCTTAAATGATGATGTTCTCTGTGTGTGTAGAGAG 7238
Db      1301 GGAAGGACGAGCTGACGCGCCCTTAAATGATGATGTTCTCTGTGTGTGTAGAGAG 1359
Qy      7239 GAAGAACTGTGGGCGTCCCTCTGCG---AGTCTCTCAAGTGCAGACCTTGGGCTC-- 7293
Db      1360 AAGCTATGTTTTGTGTATGTATGTACGATGCTGTGGAGCTGGAGACTATGGCTCGC 1419
Qy      7294 --TCTCTGCGCTCTTGGATTAACAAGCCCGGTTTGAACCACTTGTTCGA----- 7345
Db      1420 CTCGCCACCTCTCTTGAATTAACAAGCCCGGTTTGAACCACTTGTATAGCTGCA 1479
Qy      7346 -----TAAGTCTTCAAGTGTATTCAGTTCCTCTCCGCTCCCAAGTGCAGCA 7397
Db      1480 AGTGTATCTCTTTTATCTGTGTGCTCTCTCAAACTGCTCAGACACTTAAATGACAGCA 1539
Qy      7398 ATGAGACCACTGACAGATGCTGAGCTCAGCCCAAGAGGCTGGGAGACTGTGGCAGGA 7457
Db      1540 ACACCTTCTCTCTGACAGACACTGAGACTGAGCCAAAGAGGCTGGGG--GAGGCCCTAGGG 1597
Qy      7458 GACTGACGAGGACGAGGAGGACAGAGGTTGTCTCTCG---TACTTCTGAGACTGCTTC 7513
Db      1598 GAGCACCGTATGAGAGAGAGAGAGGAGGAGGCTCCAGACCTTCTTGTGAGCTGGGCTT 1657
Qy      7514 CACCTCTTGTGACGATCAGGCTCAGAGCTCAGACAGCGGGGTGAGATCA--TCCCTAATTATG 7572
Db      1658 CACTCTCCCTGCTCAGAGCTGTGGGCTCCAGCGGAGGGGTGAGAGCACTCCCTAATTATG 1717
Qy      7573 TGC--TATAAATATTCAGAGTGTATATAGAGACTATTTTCTAAGCATTTCCCTCC 7630
Db      1718 TGTATATTAATATATGTCAGATGTACATAGATCTATTTTCTAATAAATCCCTCCC 1777
Qy      7631 CTGCTCTTCTCCACTGAGTCTGG 7654
Db      1778 CACTCTCTCCCAAGAGTCTGG 1801

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RESULT 10

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US-10-264-049-756
; Sequence 756, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P413P1
; CURRENT APPLICATION NUMBER: US/10/264.049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 756
; LENGTH: 1956
; TYPE: DNA

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ORGANISM: Homo sapiens
US-10-264-049-756

Query Match 2.8%; Score 215.6; DB 16; Length 1956;

Best Local Similarity 65.6%; Pred. No. 5,7e-54;

Matches 449; Conservative 0; Mismatches 204; Indels 31; Gaps 8;

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QY 6999 AGGTATTAACAAACGGAGATCTGGAACGGGTGATGGCCGACGGCTGCTCAAG 7058
DB 1160 AGGTACTACTAAACGGAGATCTGGAACGGGTGATGGCCGACGGCTGCTCAAG 1219
QY 7059 TTGGCAAGAACTCTAGTGGCTGGAAGAAAGAGTTGAGAGAGTGGAAATTAAGA 7118
DB 1220 TTGGCAAAAACCTCAAGCGGCTGGAAGAGAGAGTTCTCCAGAGTGGAACTAGGG 1279
QY 7119 TCGGGCTGAGCCAGAGCTGATGATGATGATGATGATGATGATGATGATGATG 7178
DB 1280 TTGGAACTATACCCGGGACCAACCTCAAGAGCTGAGGCTGCAAACTTCTAGGA 1339
QY 7179 GGAAGAGAGAGCTGAGAGGCTTAAAGATGATGATGATGATGATGATGATGATG 7238
DB 1340 GGAAGAGAGAGCTGAGAGGCTTAAAGATGATGATGATGATGATGATGATGATG 1398
QY 7239 GAAGAACTGTTGGGCGTCCCTGTC--AGTCTCTCAAGTGCAGCCTTTGCGCTC-- 7293
DB 1399 AGCTGATGTTTGGTATGATGATGATGATGATGATGATGATGATGATGATG 1458
QY 7294 --TCTCTGCGCTCTTGAATTAACAAGCCCGGTTGAACCACTTGTGCA----- 7345
DB 1459 CTCGCCACCTCTCTTGAATTAACAAGCCCGGTTGAACCTTATATAGCTGA 1518
QY 7346 -----TAACCTTCCAGCTGATGATGATGATGATGATGATGATGATGATG 7397
DB 1519 AGCTGATCTCTTATCTGATGATGATGATGATGATGATGATGATGATGATG 1578
QY 7398 ATGAGACCACTGAGATGATGATGATGATGATGATGATGATGATGATGATG 7457
DB 1579 ACACCTTCTCTGAGACACTGAGTGAAGGAGGCTGAGG--GAGGCGCTAGGG 1636
QY 7458 GACTGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7513
DB 1637 GAGCACCCTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1696
QY 7514 CACTCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 7572
DB 1697 CACTCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1756
QY 7573 TGC--TATAAATATTCAGGTGATATAGAGAGCTATTTTCTAAAGCATTTCCCTCC 7630
DB 1757 TGCATATATAATATGTCAGATGATGATGATGATGATGATGATGATGATGAT 1816
QY 7631 CTGCTCTTCTCCACTGAGTGTGG 7654
DB 1817 CACTCTCTCCACAGAGTGTGG 1840

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RESULT 11

US-09-925-301-207

Sequence 207, Application US/09925301

Patent No. US20020052308A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patent Ver. 2.0

LENGTH: 1996
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-301-207

Query Match 2.8%; Score 215.6; DB 9; Length 1996;

Best Local Similarity 65.6%; Pred. No. 5.8e-54;

Matches 449; Conservative 0; Mismatches 204; Indels 31; Gaps 8;

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QY 6999 AGGTATTAACAAACGGAGATCTGGAACGGGTGATGGCCGACGGCTGCTCAAG 7058
DB 1140 AGGTACTACTAAACGGAGATCTGGAACGGGTGATGGCCGACGGCTGCTCAAG 1199
QY 7059 TTGGCAAGAACTCTAGTGGCTGGAAGAAAGAGTTGAGAGAGTGGAAATTAAGA 7118
DB 1200 TTGGCAAAAACCTCAAGCGGCTGGAAGAGAGAGTTCTCCAGAGTGGAACTAGGG 1259
QY 7119 TCGGGCTGAGCCAGAGCTGATGATGATGATGATGATGATGATGATGATGATG 7178
DB 1260 TTGGAACTATACCCGGGACCAACCTCAAGAGCTGAGGCTGCAAACTTCTAGGA 1319
QY 7179 GGAAGAGAGAGCTGAGAGGCTTAAAGATGATGATGATGATGATGATGATGATG 7238
DB 1320 GGAAGAGAGAGCTGAGAGGCTTAAAGATGATGATGATGATGATGATGATGATG 1378
QY 7239 GAAGAACTGTTGGGCGTCCCTGTC--AGTCTCTCAAGTGCAGCCTTTGCGCTC-- 7293
DB 1379 AGCTGATGTTTGGTATGATGATGATGATGATGATGATGATGATGATGATG 1438
QY 7294 --TCTCTGCGCTCTTGAATTAACAAGCCCGGTTGAACCACTTGTGCA----- 7345
DB 1439 CTCGCCACCTCTCTTGAATTAACAAGCCCGGTTGAACCTTATATAGCTGA 1498
QY 7346 -----TAACCTTCCAGCTGATGATGATGATGATGATGATGATGATGATG 7397
DB 1499 AGCTGATCTCTTATCTGATGATGATGATGATGATGATGATGATGATGATG 1558
QY 7398 ATGAGACCACTGAGATGATGATGATGATGATGATGATGATGATGATGATG 7457
DB 1559 ACACCTTCTCTGAGACACTGAGTGAAGGAGGCTGAGG--GAGGCGCTAGGG 1616
QY 7458 GACTGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7513
DB 1617 GAGCACCCTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1676
QY 7514 CACTCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 7572
DB 1677 CACTCTTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1736
QY 7573 TGC--TATAAATATTCAGGTGATATAGAGAGCTATTTTCTAAAGCATTTCCCTCC 7630
DB 1737 TGCATATATAATATGTCAGATGATGATGATGATGATGATGATGATGATGAT 1796
QY 7631 CTGCTCTTCTCCACTGAGTGTGG 7654
DB 1797 CACTCTCTCCACAGAGTGTGG 1820

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RESULT 12

US-10-131-410-64

Sequence 64, Application US/10131410

Publication No. US20030235915A1

GENERAL INFORMATION:

APPLICANT: SPECHT, THOMAS

APPLICANT: HINZMANN, BERND

APPLICANT: SCHMITT, ARMIN

APPLICANT: PILARSKY, CHRISTIAN

APPLICANT: DAHL, EDGAR

APPLICANT: ROSENTHAL, ANDRE

TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST

FILE REFERENCE: SCH-1763

CURRENT APPLICATION NUMBER: US/10/131,410

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: CURRENT FILING DATE: 2002-04-25
: PRIOR APPLICATION NUMBER: 09/646,673
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: PCT/DE99/00908
: PRIOR FILING DATE: 1999-03-19
: NUMBER OF SEQ ID NOS: 202
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 64
: LENGTH: 2269
: TYPE: DNA
: ORGANISM: Homo sapiens
: OS-10-131-410-64

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	Query Match	2.8%	Score 215.6	DB 15	Length 2269
	Best Local Similarity	65.6%	Pred. 0.5, 2e-54		
	Matches 449	Conservative 0	Mismatches 204	Indels 31	Gaps 8
QY	6999	AGTATTATCTACAAACGGGAGATCTCTGAAACGGGTGATGCGCCGACGGCTCGTCTACAA	7058		
DB	850	AGGTACTACTCAAAACGGGAGATCTCTGAAACGGGTGATGCGCGGCGACTCGTCTACAA	909		
QY	7059	TTTGGCAAGAACTCTAGTGGCTGGAAAGAAAGAAAGTTTGGAGAGATCGGAATTAAGGA	7118		
DB	910	TTTGGCAAAAACTCAMAGCGCTGGAAAGAAAGAAAGGTTCTCCAGAGTCGAACTGAGGG	969		
QY	7119	TCCGGGCTGGACCCAGGACTGACTCAGAGCAATGAATCTCAGAACTGAAGCCTTCCCTGAA	7178		
DB	970	TTGGAACTATACCCGGGACCAAACTCAGAGCACTCGAGGCTCGCAAACTTCTCTGGA	10223		
QY	7179	GGACAGGACGAGCTGACCGGCCCTTAAACATGATGTTCCCTGTGTTCTGTAGAGAG	7238		
DB	1030	GGACAGGACGAGCCAGATAG - CCCCCTCACTGGGGAATGCTCCAGCTGCTGTGTAGAG	10888		
QY	7239	GAAAGAACTGTGGGCGTGCCTCTGC - -AGTCTCTCAAGTGAAGCTTTTGGCTC - -	7293		
DB	1089	AAGCTGATGTTTGGTGTATTTGTACAGCCATGCTCTCGGAACTCGGAGACTATAGGCTTGC	1148		
QY	7294	--TCTCCCGGCCCTTTGGAATTAACAGCCCGGGTTGAACCAACTGTTCGA - - - - -	7345		
DB	1149	CTCCCAACCTCTCTTTGGAATTAACAGCCCTGGGGTTTGAAGCTGATTTATTAAGTCA	1208		
QY	7346	-----TAACTCTTCAGCTGTGATTCAGATTCCCTCCGCTCCCAATGAAGTGC	7397		
DB	1209	AGTGTATCTCTTTATATCTGGTGCTCTCTCAACCCAGATCTCAGACATTAATGACAGA	1268		
QY	7398	ATGAGACCCACTGACATGCTCTGCTCAGCCAGAGAGGCTGGGAGACTGTGACAGA	7457		
DB	1269	ACACCTTCTCTCTGAGACACCTGACATGAGCAAGAGGAGGCTGGG - -GAGGCCCTAGGG	1326		
QY	7458	GACTGCAAGGAGCGGAGGGGACAGGGTTGTGCTCG - - - -TACTCTGAGACTGCTTC	7513		
DB	1327	GAGCACCTGTATGGAGAGACAGACAGAGGGCTCCAGACCTTCTTTTGGACTGGCCCTT	1386		
QY	7514	CACCTCTTTGCTCAGTACTCAGGCTCCACAGACGGGGTTCGAGATCA -TCCCTAAATTTATG	7572		
DB	1387	CACCTCCCTGCTCAGTGTGTGGGCTCCACGGGACGGGGTCAAGACATCCTTAATTTATG	1446		
QY	7573	TGC - -TATAATATTCACGGTGTATATAGAGACTATTTTCTTAAGCAATTTCCCTCC	7630		
DB	1447	TGCTATATTAATATGTCAAGATGATCATGAGATCTATTTTCTTAACATTTCCCTCC	1506		
QY	7631	CTGCTCTTCACATGAGTGCAG 7654			
DB	1507	CACCTCTCTCCACAGAGTGTGCG 1550			

```

? APPLICANT: ARIYAMA, YUTAKA
? APPLICANT: ABURATANI, HIROYUKI
? TITLE OR INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
? FILE REFERENCE: 084335/0152
? CURRENT APPLICATION NUMBER: US/10/017,161
? CURRENT FILING DATE: 2002-12-18
? PRIOR APPLICATION NUMBER: JP 2001/246789
? PRIOR FILING DATE: 2001-06-18
? NUMBER OF SEQ ID NOS: 2430
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1953
? LENGTH: 1435
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: source
? LOCATION: (1)..(1435)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (201)..(1235)
? FEATURE:
? NAME/KEY: modified_base
? LOCATION: (1040)..(1139)
? OTHER INFORMATION: a, t, c, g, unknown or other
? FEATURE:
? NAME/KEY: modified_base
? LOCATION: (1145)
? OTHER INFORMATION: a, t, c, g, unknown or other
? US-10-017-161-1953

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	Query Match	2.4%;	Score 185.8;	DB 15;	Length 1435;
	Best Local Similarity	79.4%;	Pred. No. 6,16-45;		
	Matches	220;	Conservative	0;	Mismatches 57; Indels 0; Gaps 0;
Qy	6181	TTGGGATATGAGAGCCAGGTCGCTCTAGAGAGAGGGGACCCACAGACTGATAACTGAG			62410
Db	442	TGGGGCGGGCGAGGGCTGAGCTGCCTCTTGGGTAGAGGGGACACTTGGAGTGGCAACTGATG			383
Qy	6241	AAATCTTCCTCTTAGGCCCCCAGAGTACTCACCCTGTGGAGTTATCCGAGATCCTTA			63000
Db	382	GAGGCTGGCCTTTCGAGGGGCCAGAGGCCACCACTGTGGAGTTTCATCCGGGACATCTTC			323
Qy	6301	ATTCACCCCCAGCTCAGAGAAAGGCTCATGAACTGGGAGAAACGGGACGAGAGTGTCTTC			63666
Db	322	ATTCACCCCGAGCTCAGAGAGGCTCATGAACTGGGAGAAATGGCAATGAAAGGCGTCTTC			263
Qy	6361	AAGTTTCTTCGCTCAGAGGCGTGGGCCCACTCGGGGCGAGAAAGAAACAGCAAC			64200
Db	262	AAGTTCCTCGGCGCTCGAGGCTGTGGCCCACTATGGGGCCAAAAGAAAAGAACGCAAC			203
Qy	6421	ATGACCTATGAGAAAGCTGAGCCGAGCCATGAGGTGAG			6457
Db	202	ATGACCTTACGAGAAAGCTGAGCCGGGACCATGAGGTGAG			166

RESULT13
US-10-017-161-1953/c
; Sequence 1953, Application US/10017164
; Publication No. US20030145668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI

```

RESULT 14
US-10-292-798-1601/c
: Sequence 1601, Application US/10292798
: Publication No. US20030235833A1
: GENERAL INFORMATION:
: APPLICANT: SUMA, MAKIKO
: APPLICANT: ASAI, KIYOSHI
: APPLICANT: AKIYAMA, YUTAKA
: APPLICANT: ABRARANI, HIROYUKI
: TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING
: FILE REFERENCE: 08435/166
: CURRENT APPLICATION NUMBER: US/10/292,798
: PRIOR FILING DATE: 2002-11-13
: PRIOR APPLICATION NUMBER: 10/017,161
: PRIOR FILING DATE: 2001-12-18
: PRIOR APPLICATION NUMBER: JP 2001-246789
: PRIOR FILING DATE: 2001-06-18
: NUMBER OF SEQ. ID NOS: 2070

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SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1601
; LENGTH: 1435
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1435)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1235)
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1040)..(1139)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1145)..(1145)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-292-798-1601

Query Match 2.4%; Score 185.8; DB 15; Length 1435;
Best Local Similarity 79.4%; Pred. No. 6.1e-45;
Matches 220; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 6181 TTGGGATAGAGAGGCCAGTCCCTTAGAGAGAGGGGACCCACAGACTGATACTGAGG 6240
DB 442 TGGGGGGGGGGGGCTGGCTGCTCCCTTGGGAGAGGGGACACTTGGAGCAACTGATG 383
QY 6241 AATCTTCCCTTAGAGGCCAGAGGTACTACCTGTGGAGTTTATCCGAGACATCTTA 6300
DB 382 GAGGCTGGCTTTCAGAGGCCAGAGGACCCACCTGTGGAGTTTCATCCGGACATCTTC 323
QY 6301 ATCCACCCGAGCTCAACGAGGCTTCATGAGTGGAGAACCCGCAAGAGGCTGTTC 6360
DB 322 ATCCACCCGAGCTCAACGAGGCTTCATGAGTGGAGAACCCGCAAGAGGCTGTTC 263
QY 6361 AAGTTTCTTGGCTCAAGAGGCCGTGGCCCACTCTGGGGCCAGAAAGAAAGACAGAAC 6420
DB 262 AAGTTTCTTGGCTCAAGAGGCCGTGGCCCACTCTGGGGCCAGAAAGAAAGACAGAAC 203
QY 6421 ATGACCTATGAGAGGCTGAGCCGAGCCATGAGGTGAG 6457
DB 202 ATGACCTATGAGAGGCTGAGCCGAGCCATGAGGTGAG 166

RESULT 15

US-10-425-115-58949/C
; Sequence 58949, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21 (53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 58949
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(229)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_153757C.1
US-10-425-115-58949

Query Match 2.3%; Score 179; DB 18; Length 229;
Best Local Similarity 93.7%; Pred. No. 2.5e-43;
Matches 208; Conservative 0; Mismatches 11; Indels 3; Gaps 2;

QY 7532 TCAGGCTCCACAGACGGGGGTGGATCATCCCTAATTATGTGCTATTAATTTCCA-CG 7590
DB 229 TCGGGCTCCNCAAGCCGGGGGTGGATCATCCCTAATTATGTGCTATTAATTTCCAAGG 170
QY 7591 TGTATATAGAGACTATTTTCTTAAAGATTTCCCTCCCTGCTCTTCTCCAGTAGTG 7650
DB 169 TGTATATAGAGACTATTTTCTTAAAGATTTCCCTCCCTGCTCTTCTCCAGTAGTG 110
QY 7651 CTGGTGCCAGACTGATTTTCTTAAAGATTTCCCTCCCTGCTCTTCTCCAGTAGTG 7710
DB 109 CTGGTGCCAGACTGATTTTCTTAAAGATTTCCCTCCCTGCTCTTCTCCAGTAGTG 52
QY 7711 ATTCAGAGCCCTCTTCCCTCCAGAGGGGTCTCTGATCC 7752
DB 51 ATTCAGAGCCCTCTTCCCTCCAGAGGGGTCTCTGATCC 10

Search completed: November 15, 2004, 23:09:03
Job time : 3642.71 secs

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QY 7294 --TCTCTGCGCCCTCTGGAATTACAAGCCCGGTTTGAACCACTTGT----- 7241
DB 1394 CTCGCCACCTCTCTCTTGGAATTACAAGCCCTGGGTTTGAAGTGACTTTATAGCTGCA 1453
QY 7342 --TCGATTAATCTCTTCAGCTGTGATTCAGATTCCCTCCGTCACCATGAGCTGCAAT 7399
DB 1454 AGTATATCTCTCTTTATCTGTGCTCTCTCAAACTCCAGTCTCAGACACTTAAATGACAG 1513
QY 7400 GAGAC---CCACCTGAGATGCTGCTGAGCCCAAGAGAGGAGGAGAGCTGTGGAGG 7456
DB 1514 AACACCTCTCTCTGAGACACTTGGACTGAGCCCAAGAGGAGGCTGGAGGCTCT---AG 1569
QY 7457 AGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7513
DB 1570 GAGACACCGTGTGATGAGAGAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1629
QY 7514 CACCTCTTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 7572
DB 1630 CACCTCTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1689
QY 7573 TGCATTA--AATATTCAGAGTATATAGAGAGTATTTTCTAAAGCATTTCCCTCC 7630
DB 1690 TGCATTAATAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1749
QY 7631 CTGCTCTTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 7654
DB 1750 CACTCTCTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1773

RESULT 2

US-09-570-593-4
; Sequence 4, Application US/09570593
; Patent No. 6566063
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xun, Hong
; APPLICANT: Hartowe, Greg
; TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 2300-1556
; CURRENT APPLICATION NUMBER: US/09/570,593
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PaetSeq for windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1211)
; OTHER INFORMATION: Human epithelial-restricted with serine box (ESX)
; OTHER INFORMATION: protein.
US-09-570-593-4

Query Match 2.88; Score 216; DB 4; Length 1907;
Best Local Similarity 66.7%; Pred. No. 2.2e-52;
Matches 456; Conservative 0; Mismatches 195; Indels 33; Gaps 9;
QY 6999 AGGTATTACTACAAACGAGAGATCTGGAACGGGTGATGGCCGAGCGCTGCTTACAAG 7058
DB 1095 AGGTACTACTACAAACGAGAGATCTGGAACGGGTGATGGCCGAGCGCTGCTTACAAG 1154
QY 7059 TTTGGCAAGAACTCTAGTGGCTGGAAGGAAGAGAGGTTGGAGAGTCCGAAATTAAGA 7118
DB 1155 TTTGGCAAAACTCAACGGCTGGAAGGAAGAGAGGTTTCCAGAGTCCGAAACTGAGGG 1214
QY 7119 TCGGGGCTGAGCCAGAGCTGATCTGAGGCTGAGTGAATCTCCAGAACTGAAGCTTCTGGA 7178
DB 1215 TTGGAATTAATACCGGAGCAAACTCAAGGACCACTGAGGCTTGCAAACTTCTGGA 1274

QY 7179 GAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7238
DB 1275 GAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1333
QY 7239 GAAAGAACTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7293
DB 1334 AACCTGATGTTTGGTGTATGTCACCATGCTGCTTGGAGCTGAGAGTATGAGCTGAG 1393
QY 7294 --TCTCTGCGCCCTCTGGAATTACAAGCCCGGTTTGAACCACTTGT----- 7341
DB 1394 CTCGCCACCTCTCTCTTGGAATTACAAGCCCTGGGTTTGAAGTGACTTTATAGCTGCA 1453
QY 7342 --TCGATTAATCTCTTCAGCTGTGATTCAGATTCCCTCCGTCACCATGAGCTGCAAT 7399
DB 1454 AGTATATCTCTCTTTATCTGTGCTCTCTCAAACTCCAGTCTCAGACACTTAAATGACAG 1513
QY 7400 GAGAC---CCACCTGAGATGCTGCTGAGCCCAAGAGAGGAGGAGGAGGAGGAGGAGG 7456
DB 1514 AACACCTCTCTCTGAGACACTTGGACTGAGCCCAAGAGGAGGAGGAGGAGGAGGAGG 1569
QY 7457 AGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7513
DB 1570 GAGACACCGTGTGATGAGAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1629
QY 7514 CACCTCTTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 7572
DB 1630 CACTCTCTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1689
QY 7573 TGCATTA--AATATTCAGAGTATATAGAGAGTATTTTCTAAAGCATTTCCCTCC 7630
DB 1690 TGCATTAATAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1749
QY 7631 CTGCTCTTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 7654
DB 1750 CACTCTCTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1773

RESULT 3

US-08-746-789A-1
; Sequence 1, Application US/08746789A
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismaili, Martin J. Tyms, Christine DeBouck
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELP3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,789A
; FILING DATE: No. 5789200elember 15, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG 50024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5219
; TELEFAX: 610 270 4026
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1920
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 ANTI-SENSE: No
 US-08-746-789A-1

Query Match 2.8%; Score 215.6; DB 1; Length 1920;
 Best Local Similarity 65.6%; Pred. No. 2.9e-52;
 Matches 449; Conservative 0; Mismatches 204; Indels 31; Gaps 8;

6999 AGGTATTACTACAAAGGAGATCTGGAACGGGTGATGGCGAGCGCTCTCAAG 7058
 1114 AGGTACTACTACAAAGGAGATCTGGAACGGGTGATGGCGAGCGCTCTCAAG 1173
 7059 TTTGGAGAAGCTCTAGTGGCTGGAAGAAAGAGTTGAGAGAGTGGAAATTAGA 7118
 1174 TTTGGCAAAACTCAAGCGGCTGGAAGAGAAAGAGTTCTCCAGAGTCGAAGTGA 1233
 7119 TCGGGCTGAGACCCAGAGACTGATCAGCATGAATCCCAAGTCTCCGGA 7178
 1234 TTGGAATATATACCGGAGCAAACTCAAGCACTGAGGCTGCAAACTTCTGGA 1293
 7179 GACAGGCAAGGCTGAGCGGCTTAACTGATGTTCCCTGTTGTTCTGTAAGAG 7238
 1294 GACAGGCAAGGCTGAGCGGCTTAACTGATGTTCCCTGTTGTTCTGTAAGAG 1352
 7239 GAAGAACTGTTGGGCGTGGCTCTGCG--AGTCTCTCAAGTGCAGGCTTTGGCTC-- 7293
 1353 AAGCTGATGTTTGGTATTTGTCAGCATGTCCTGAGACTGAGAGATGAGCTCGC 1412
 7294 --TCTCTGCGCTTCTGGAATTAACAAGCCCGGTTGAACCACTTTGCA----- 7345
 1413 CTCCTCAACCTCTCTGGAATTAACAAGCCCGGTTGAACCTGATGATGCTGCA 1472
 7346 -----TACTCTTCAGCTGATGATTCAGTTCCCTCCGTCCTCAACTGAGCTGCA 1472
 1473 AGGTATCTCTTTTATCTGTCCTCTCAAAACCGATCTGAGACACTAAATGACAGA 1532
 7398 ATGAGACCACTGAGAGTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7457
 1533 ACACCTTCTCTGAGACACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1590
 7458 GACTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7513
 1591 GAGCACCCTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1650
 7514 CACTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7572
 1651 CACTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1710
 7573 TGC--TATAATATTCAGGTTATATAGAGATATTTTCTAAAGCATTTCCCTCC 7630
 1711 TGTAT 1770
 7631 CTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7654
 1771 CACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1794

RESULT 4
 US-09-389-681-282
 ; Sequence 282, Application US/09389681A
 ; Patent No. 6518237
 ; GENERAL INFORMATION:
 ; APPLICANT: Yugui, Jiang
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.470C3

CURRENT APPLICATION NUMBER: US/09/389,681A
 ; CURRENT FILING DATE: 1999-09-02
 ; NUMBER OF SEQ ID NOS: 463
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 282
 ; LENGTH: 502
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-389-681-282

Query Match 2.1%; Score 163.8; DB 4; Length 502;
 Best Local Similarity 88.9%; Pred. No. 1.7e-37;
 Matches 177; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

6256 GCGCCAGAGGATCTACCTGAGGAGTTATCCAGATCTATCCACCCGAGCTC 6315
 258 GCGCCAGAGGATCTACCTGAGGAGTTATCCAGATCTATCCACCCGAGCTC 6317
 6316 AACGAGGCTCATGAGTGGAGAAACCGGACGAGGCTGTTCAAGTTCTTCCCTCA 6375
 318 AACGAGGCTCATGAGTGGAGAAATCGGATGAAAGGCTTCAAGTTCTTCCCTCC 377
 6376 GAGGCGTGGCCCACTTGGGCGCAGAGAAAGAGAAACAGCAATGACTATGAGAG 6435
 378 GAGGCGTGGCCCACTTGGGCGCAGAGAAAGAGAAACAGCAATGACTATGAGAG 6437
 6436 CTGAGCGGAGCCATGAGGT 6454
 438 CTGAGCGGAGCCATGAGGT 456

RESULT 5
 US-09-620-405B-282
 ; Sequence 282, Application US/09620405B
 ; Patent No. 6528054
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Yugui
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Hepler, William T.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.470C8
 ; CURRENT APPLICATION NUMBER: US/09/620,405B
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 495
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 282
 ; LENGTH: 502
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-620-405B-282

Query Match 2.1%; Score 163.8; DB 4; Length 502;
 Best Local Similarity 88.9%; Pred. No. 1.7e-37;
 Matches 177; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

6256 GCGCCAGAGGATCTACCTGAGGAGTTATCCAGATCTATCCACCCGAGCTC 6315
 258 GCGCCAGAGGATCTACCTGAGGAGTTATCCAGATCTATCCACCCGAGCTC 6317
 6316 AACGAGGCTCATGAGTGGAGAAACCGGACGAGGCTGTTCAAGTTCTTCCCTCA 6375
 318 AACGAGGCTCATGAGTGGAGAAATCGGATGAAAGGCTTCAAGTTCTTCCCTCC 377
 6376 GAGGCGTGGCCCACTTGGGCGCAGAGAAAGAGAAACAGCAATGACTATGAGAG 6435
 378 GAGGCGTGGCCCACTTGGGCGCAGAGAAAGAGAAACAGCAATGACTATGAGAG 6437
 6436 CTGAGCGGAGCCATGAGGT 6454

Db 438 CTGAGCCGGGCATGAGGT 456

RESULT 6

US-09-339-338-282
Sequence 282, Application US/09339338A
Patent No. 6573368

GENERAL INFORMATION:

APPLICANT: Yugui, Jiong

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.470C2

CURRENT APPLICATION NUMBER: US/09/339,338A

CURRENT FILING DATE: 1999-06-23

NUMBER OF SEQ ID NOS: 315

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 282

LENGTH: 502

TYPE: DNA

ORGANISM: Homo sapiens

US-09-339-338-282

Query Match 2.1%; Score 163.8; DB 4; Length 502;

Best Local Similarity 88.9%; Pred. No. 1.7e-37;

Matches 177; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

6256 GCGCCAGAGTACTACCTGTGGAGTTATCCGAGACATCTTAATCCACCCGAGCTC 6315

258 GCGCCAGAGGACCCACCTGTGGAGTTATCCGAGACATCTTAATCCACCCGAGCTC 317

6316 AACGAGGCTCTCATGAAATGGGAGAACCGGACGAGGCTGTGTTCAAGTTCTTCCGCTCA 6375

318 AACGAGGCTCTCATGAAATGGGAGAACCGGACGAGGCTGTGTTCAAGTTCTTCCGCTC 377

6376 GAGGCGGTGGCCCACTCTGGGGCCAGAGAAAGAGAAACAGCAATGACCTATGAGAAG 6435

378 GAGGCTGTGGCCCACTATGAGGCGCCAAAGAAAGAAAGAAAGCAATGACCTATGAGAAG 437

6436 CTGAGCCGAGCCATGAGGT 6454

438 CTGAGCCGGGCATGAGGT 456

RESULT 7

US-09-433-826B-282

Sequence 282, Application US/09433826B

Patent No. 6579973

GENERAL INFORMATION:

APPLICANT: Jiong, Yugui

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.470C4

CURRENT APPLICATION NUMBER: US/09/433,826B

CURRENT FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 474

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 282

LENGTH: 502

TYPE: DNA

ORGANISM: Homo sapiens

US-09-433-826B-282

Query Match 2.1%; Score 163.8; DB 4; Length 502;

Best Local Similarity 88.9%; Pred. No. 1.7e-37;

Matches 177; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 6256 GCGCCAGAGTACTACCTGTGGAGTTATCCGAGACATCTTAATCCACCCGAGCTC 6315

258 GCGCCAGAGGACCCACCTGTGGAGTTATCCGAGACATCTTAATCCACCCGAGCTC 317

6316 AACGAGGCTCTCATGAAATGGGAGAACCGGACGAGGCTGTGTTCAAGTTCTTCCGCTCA 6375

318 AACGAGGCTCTCATGAAATGGGAGAACCGGACGAGGCTGTGTTCAAGTTCTTCCGCTC 377

6376 GAGGCGGTGGCCCACTCTGGGGCCAGAGAAAGAGAAACAGCAATGACCTATGAGAAG 6435

378 GAGGCTGTGGCCCACTATGAGGCGCCAAAGAAAGAAAGAAAGCAATGACCTATGAGAAG 437

6436 CTGAGCCGAGCCATGAGGT 6454

438 CTGAGCCGGGCATGAGGT 456

RESULT 8

US-09-604-287A-282

Sequence 282, Application US/09604287A

Patent No. 6586572

GENERAL INFORMATION:

APPLICANT: Jiong, Yugui

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.470C7

CURRENT APPLICATION NUMBER: US/09/604,287A

CURRENT FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 489

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 282

LENGTH: 502

TYPE: DNA

ORGANISM: Homo sapiens

US-09-604-287A-282

Query Match 2.1%; Score 163.8; DB 4; Length 502;

Best Local Similarity 88.9%; Pred. No. 1.7e-37;

Matches 177; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

6256 GCGCCAGAGTACTACCTGTGGAGTTATCCGAGACATCTTAATCCACCCGAGCTC 6315

258 GCGCCAGAGGACCCACCTGTGGAGTTATCCGAGACATCTTAATCCACCCGAGCTC 317

6316 AACGAGGCTCTCATGAAATGGGAGAACCGGACGAGGCTGTGTTCAAGTTCTTCCGCTCA 6375

318 AACGAGGCTCTCATGAAATGGGAGAACCGGACGAGGCTGTGTTCAAGTTCTTCCGCTC 377

6376 GAGGCGGTGGCCCACTCTGGGGCCAGAGAAAGAGAAACAGCAATGACCTATGAGAAG 6435

378 GAGGCTGTGGCCCACTATGAGGCGCCAAAGAAAGAAAGAAAGCAATGACCTATGAGAAG 437

6436 CTGAGCCGAGCCATGAGGT 6454

438 CTGAGCCGGGCATGAGGT 456

RESULT 9

US-09-834-759-282

Sequence 282, Application US/09834759

Patent No. 6680197

GENERAL INFORMATION:

APPLICANT: Jiong, Yugui

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun

APPLICANT: Harlocker, Susan L.

APPLICANT: Hepler, William T.

Query Match 2.1%; Score 163.8; DB 4; Length 502;

Best Local Similarity 88.9%; Pred. No. 1.7e-37;

Matches 177; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834.759
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-09-834-759-282

Query Match 2.1%; Score 163.8; DB 4; Length 502;
Best Local Similarity 88.9%; Pred. No. 1.7e-37;
Matches 177; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6256 GCCCCAGAGTACTACCTGTGGAGTTATCCGAGACATCCATCCACCCGAGCTC 6315
DB 258 GCCCCAGAGACACCCACTGTGGAGTTATCCGAGACATCCATCCACCCGAGCTC 317
QY 6316 AACGAAGCCTCATGAAGTGGAGAACCGGACAGAGGCTGTTCAGATTCTTCGCTCA 6375
DB 318 AACGAGGCTCATGAAGTGGAGAACCGGACATGAGCGCTTCAGATTCTTCGCTCC 377
QY 6376 GAGGCGGTGGCCCAACTCTGGGCGCAGAGAAGAACGAAACATGACTATGAGAAG 6435
DB 378 GAGGCTGTGGCCCAACTCATGTGGGCGCAAAAAGAAAGAACATGACTATGAGAAG 437
QY 6436 CTGAGCCGAGCAGTGAAGT 6454
DB 438 CTGAGCCGAGCAGTGAAGT 456

RESULT 10
US-09-590-751A-282
Sequence 282, Application US/09590751A
Patent No. 6756477
GENERAL INFORMATION:
APPLICANT: Yuqun, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C6
CURRENT APPLICATION NUMBER: US/09/590.751A
CURRENT FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 479
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-09-590-751A-282

Query Match 2.1%; Score 163.8; DB 4; Length 502;
Best Local Similarity 88.9%; Pred. No. 1.7e-37;
Matches 177; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6256 GCCCCAGAGTACTACCTGTGGAGTTATCCGAGACATCCATCCACCCGAGCTC 6315
DB 258 GCCCCAGAGACACCCACTGTGGAGTTATCCGAGACATCCATCCACCCGAGCTC 317
QY 6316 AACGAAGCCTCATGAAGTGGAGAACCGGACAGAGGCTGTTCAGATTCTTCGCTCA 6375
DB 318 AACGAGGCTCATGAAGTGGAGAACCGGACATGAGCGCTTCAGATTCTTCGCTCC 377
QY 6376 GAGGCGGTGGCCCAACTCTGGGCGCAGAGAAGAACGAAACATGACTATGAGAAG 6435
DB 378 GAGGCTGTGGCCCAACTCATGTGGGCGCAAAAAGAAAGAACATGACTATGAGAAG 437

QY 6436 CTGAGCCGAGCAGTGAAGT 6454
DB 438 CTGAGCCGAGCAGTGAAGT 456

RESULT 11
US-09-016-434-927
Sequence 927, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 927:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNCR101
CLONE: 773734
US-09-016-434-927

Query Match 1.6%; Score 125.6; DB 4; Length 237;
Best Local Similarity 79.3%; Pred. No. 1.6e-26;
Matches 149; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 6999 AGGTATTACTACAAACGAGATCTGTGAACGGGTGATGGCCGAGCGCTCTCAAG 7058
DB 50 AGGTATTACTACAAACGAGATCTGTGAACGGGTGATGGCCGAGCGCTCTCAAG 109
QY 7059 TTTGGCAAGACTCTAGTGGCTGGAAGGAAGAGTTGAGAGAGTGAATTAAAGA 7118
DB 110 TTTGGCAAAACCTCAAGCGGCTGGAAGGAAGAGTTCTCAAGTGGAACTGAAGG 169
QY 7119 TCGGGGCTGAGCCGAGACCTGACTGAGCATGAATCCAGAACTGAAGCTTCTGAA 7178
DB 170 TTGGAATCTATCCCGGACCAAACTACGAGACCACTCGAGGCTCTGCAACTTCTCGGA 229
QY 7179 GGACAGGC 7186
DB 230 GGACAGGC 237

RESULT 12
US-09-245-041-4
Sequence 4, Application US/09245041
Patent No. 6274339
GENERAL INFORMATION:
APPLICANT: Moore, K.
APPLICANT: Nagle, D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
FILE REFERENCE: 7853-136
CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER FILING DATE: 1998-07-21
EARLIER APPLICATION NUMBER: 60/104,978
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 5973
TYPE: DNA
ORGANISM: Mus musculus
US-09-245-041-4

Query Match 1.6%; Score 123.6; DB 3; Length 5973;
Best Local Similarity 67.4%; Pred. No. 8.3e-25;
Matches 174; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 1841 TTGTTCTGAGTTTGTAGTTTTCAGACAGAGTTCTGTGTAGCCCTGGCTGTCTG 1900
DB 5390 TTCTTTTTCATTTTCGTTTTCAGACAGAGTTCTGTGTAGCCCTGGCTGTCTG 5449
QY 1901 GAACCTACTGTGACAGAGCTGGCTGCTGAATCTGAGAAATCTTCTACTCTACTTCA 1960
DB 5450 GAACCTACTGTGACAGAGCTGGCTGCTGAATCTGAGAAATCTTCTACTCTACTTCA 5509
QY 1961 GAGTGTGGATTAAGATGTGCGCTGCTCTCCACCCCAATTTGTTTGTGTTT 2020
DB 5510 AATGCTGGATTAAGATGTGCGCTGCTCTCCACCCCAATTTGTTTGTGTTT 5569
QY 2021 AGGGCCCCGGTAAACAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2080
DB 5570 ATATATTTCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5629
QY 2081 TGTGGGCTTGTGACCAC 2098
DB 5630 CATTTTTCATTCTTAC 5647
US-09-245-041-4

RESULT 13
US-09-358-055B-4
Sequence 4, Application US/09358055B
Patent No. 6713277
GENERAL INFORMATION:
APPLICANT: Moore, K.
APPLICANT: Nagle, D.L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS INCLUDING
TITLE OF INVENTION: OBESITY
FILE REFERENCE: 7853-151
CURRENT APPLICATION NUMBER: US/09/358,055B
CURRENT FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: 09/245,041
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 153
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 5973
TYPE: DNA
ORGANISM: Mus musculus
US-09-358-055B-4

Query Match 1.6%; Score 123.6; DB 4; Length 5973;
Best Local Similarity 67.4%; Pred. No. 8.3e-25;
Matches 174; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 1841 TTGTTCTGAGTTTGTAGTTTTCAGACAGAGTTCTGTGTAGCCCTGGCTGTCTG 1900
DB 5390 TTCTTTTTCATTTTCGTTTTCAGACAGAGTTCTGTGTAGCCCTGGCTGTCTG 5449
QY 1901 GAACCTACTGTGACAGAGCTGGCTGCTGAATCTGAGAAATCTTCTACTCTACTTCA 1960
DB 5450 GAACCTACTGTGACAGAGCTGGCTGCTGAATCTGAGAAATCTTCTACTCTACTTCA 5509
QY 1961 GAGTGTGGATTAAGATGTGCGCTGCTCTCCACCCCAATTTGTTTGTGTTT 2020
DB 5510 AATGCTGGATTAAGATGTGCGCTGCTCTCCACCCCAATTTGTTTGTGTTT 5569
QY 2021 AGGGCCCCGGTAAACAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2080
DB 5570 ATATATTTCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5629
QY 2081 TGTGGGCTTGTGACCAC 2098
DB 5630 CATTTTTCATTCTTAC 5647
US-09-245-041-4

RESULT 14
US-09-893-238-4
Sequence 4, Application US/09893238
Patent No. 672348
GENERAL INFORMATION:
APPLICANT: Moore, K.
APPLICANT: Nagle, D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
FILE REFERENCE: 7853-237
CURRENT APPLICATION NUMBER: US/09/893,238
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 09/245,041
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/093,630
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: 60/104,978
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 5973
TYPE: DNA
ORGANISM: Mus musculus
US-09-893-238-4

Query Match 1.6%; Score 123.6; DB 4; Length 5973;
Best Local Similarity 67.4%; Pred. No. 8.3e-25;
Matches 174; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 1841 TTGTTCTGAGTTTGTAGTTTTCAGACAGAGTTCTGTGTAGCCCTGGCTGTCTG 1900
DB 5390 TTCTTTTTCATTTTCGTTTTCAGACAGAGTTCTGTGTAGCCCTGGCTGTCTG 5449
QY 1901 GAACCTACTGTGACAGAGCTGGCTGCTGAATCTGAGAAATCTTCTACTCTACTTCA 1960
DB 5450 GAACCTACTGTGACAGAGCTGGCTGCTGAATCTGAGAAATCTTCTACTCTACTTCA 5509
QY 1961 GAGTGTGGATTAAGATGTGCGCTGCTCTCCACCCCAATTTGTTTGTGTTT 2020
DB 5510 AATGCTGGATTAAGATGTGCGCTGCTCTCCACCCCAATTTGTTTGTGTTT 5569
QY 2021 AGGGCCCCGGTAAACAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2080
DB 5570 ATATATTTCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5629
QY 2081 TGTGGGCTTGTGACCAC 2098
US-09-893-238-4

Db 5630 CATTTCATCTAC 5647

RESULT 15
US-09-020-956-44/c
; Sequence 44, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 852 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-020-956-44

Query Match 1.5%; Score 115.4; DB 3; Length 852;
Best local Similarity 74.1%; Pred. No. 4.5e-23;
Matches 146; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 6258 CCCGAGGTAATCTACCTGTGGAGTTATCCGAGACATCTAATCCACCCGAGCTCAA 6317
DB 401 CCCGAGAGGAGCTACCTATATGGAATTCATCCGACATCTCTTGAACCCAGCAAGAA 342
QY 6318 CGAAGCCTCATGAAGTGGAGAACCGGACGAGGGGTGTTCAGTTTCTTCGCTCAGA 6377
DB 341 CCCAGATTATATTAATAATGGGAAGACCGATCTGAGGGGCTTTCAGTTCTTGAATCAGA 282
QY 6378 GGCCTGGCCCACTCTGGGGCCAGAAAGAGAGAACAGCAATGACCTATGAGAAGCT 6437
DB 281 GGCAGTGGCTCAGCTATGGGTAAGAAAGAAACACAGACATGACCTATGAAAAGCT 222
QY 6438 GAGCCGAGCCATGAGGT 6454
DB 221 CAGCCGAGCTATGAGAT 205

Search completed: November 15, 2004, 14:14:15
Job time : 658.884 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:42:48 ; Search time 9.84905 Seconds
(without alignments)
11515.905 Million cell updates/sec

Title: US-08-978-217-14

Perfect score: 21

Sequence: 1 GTACCTCATGCGCCGGCTCAG 21

Scoring table: IDENTITY_NUC

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/prodata/1/pubpna/PCF_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/PCFUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	100.0	237	16	US-10-305-720-927	Sequence 927, App
C 2	100.0	451	9	US-09-998-598-32	Sequence 32, Appl
C 3	100.0	499	9	US-09-998-598-2290	Sequence 2290, Ap
C 4	100.0	502	9	US-09-604-287A-282	Sequence 282, App
C 5	100.0	502	9	US-09-834-759-282	Sequence 282, App
C 6	100.0	502	9	US-09-339-338-282	Sequence 282, App
C 7	100.0	502	10	US-09-551-621-282	Sequence 282, App
C 8	100.0	502	13	US-10-007-805-282	Sequence 282, App
C 9	100.0	502	14	US-10-076-622-282	Sequence 282, App
C 10	100.0	502	15	US-10-124-805-282	Sequence 282, App
C 11	100.0	1907	14	US-10-097-340-74	Sequence 74, Appl
C 12	100.0	1907	15	US-10-291-808-27	Sequence 27, Appl

C 13	21	100.0	1915	9	US-09-964-824A-101	Sequence 101, App
C 14	21	100.0	1915	9	US-09-964-824A-563	Sequence 563, App
C 15	21	100.0	1915	9	US-09-880-107-3420	Sequence 3420, Ap
C 16	21	100.0	1915	9	US-09-967-768A-192	Sequence 192, App
C 17	21	100.0	1917	9	US-09-922-217-1105	Sequence 1105, Ap
C 18	21	100.0	1917	13	US-10-025-380-1105	Sequence 1105, Ap
C 19	21	100.0	1956	16	US-10-264-009-756	Sequence 756, App
C 20	21	100.0	1996	9	US-09-925-301-207	Sequence 207, App
C 21	21	100.0	2269	15	US-10-131-410-64	Sequence 64, Appl
C 22	19	100.0	275	14	US-10-060-036-3261	Sequence 3261, Ap
C 23	19	90.5	1435	15	US-10-017-161-1853	Sequence 1953, Ap
C 24	19	90.5	1435	15	US-10-292-798-1601	Sequence 1601, Ap
C 25	17.4	82.9	1839	17	US-10-437-963-82892	Sequence 82892, A
C 26	16.8	80.0	7813	10	US-09-854-867-27	Sequence 27, Appl
C 27	16.8	80.0	9025608	15	US-10-156-761-1	Sequence 1, Appl
C 28	16.4	78.1	619	15	US-10-291-172-388	Sequence 388, App
C 29	16.4	78.1	619	13	US-10-221-278-388	Sequence 388, App
C 30	16.4	78.1	733	16	US-10-027-633-149050	Sequence 149050,
C 31	16.4	78.1	733	15	US-10-027-633-149050	Sequence 528, App
C 32	16.4	78.1	1629	16	US-10-641-643-528	Sequence 5633, Ap
C 33	16.4	78.1	1851	15	US-10-156-761-5632	Sequence 10965,
C 34	16.4	78.1	2034	13	US-10-027-633-109965	Sequence 109965,
C 35	16.4	78.1	2034	15	US-10-027-633-109965	Sequence 599, App
C 36	16.4	78.1	2212	9	US-09-919-497-25	Sequence 25, Appl
C 37	16.4	78.1	2450	16	US-10-388-934-599	Sequence 599, App
C 38	16.4	78.1	10322	9	US-09-764-868-1471	Sequence 1471, Ap
C 39	16.4	78.1	130427	14	US-10-175-523-87	Sequence 87, Appl
C 40	16.4	78.1	9025608	15	US-10-156-761-1	Sequence 1, Appl
C 41	16.2	77.1	366	15	US-10-187-267A-10	Sequence 10, Appl
C 42	16.2	77.1	402	16	US-10-242-533A-7139	Sequence 7139, Ap
C 43	16.2	77.1	402	16	US-10-085-783A-7139	Sequence 7139, Ap
C 44	16.2	77.1	470	16	US-10-242-533A-42404	Sequence 42404, A
C 45	16.2	77.1	470	16	US-10-085-783A-42404	Sequence 42404, A

ALIGNMENTS

RESULT 1
US-10-305-720-927/c
; Sequence 927, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OR INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305, 720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016, 434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 927
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040010136A1 773734
US-10-305-720-927

Query Match 100.0%; Score 21; DB 16; Length 237;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 55 GTACCTCATGCGCCGGCTCAG 21
1 GTACCTCATGCGCCGGCTCAG 21

RESULT 2
US-09-998-598-32/c
; Sequence 32, Application US/0998598

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; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 32
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-998-598-32
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Query Match          100.0%; Score 21; DB 9; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTACTCATGCGCCGGCTCAG 21
Db 109 GTACTCATGCGCCGGCTCAG 89
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RESULT 3
US-09-998-598-2290
; Sequence 2290, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 2290
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-998-598-2290
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Query Match          100.0%; Score 21; DB 9; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTACTCATGCGCCGGCTCAG 21
Db 156 GTACTCATGCGCCGGCTCAG 176
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RESULT 4
US-09-604-287A-282/c
; Sequence 282, Application US/09604287A
; Patent No. US20020064872A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuguo
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
```

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; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-604-287A-282
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Query Match          100.0%; Score 21; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTACTCATGCGCCGGCTCAG 21
Db 458 GTACTCATGCGCCGGCTCAG 438
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RESULT 5
US-09-834-759-282/c
; Sequence 282, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuguo
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-834-759-282
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Query Match          100.0%; Score 21; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTACTCATGCGCCGGCTCAG 21
Db 458 GTACTCATGCGCCGGCTCAG 438
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RESULT 6
US-09-339-338-282/c
; Sequence 282, Application US/09339338A
; Patent No. US20020102602A1
; GENERAL INFORMATION:
; APPLICANT: Yuguo, Jiang
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-339-338-282

Query Match 100.0%; Score 21; DB 9; Length 502;

Best Local Similarity 100.0%; Pred. No. 0.95; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21

DB 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 7

US-09-551-621-282/c

; Sequence 282, Application US/09551621

; Publication No. US20030104366A1

; GENERAL INFORMATION:

; APPLICANT: Yuqin, Jiang

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; FILE REFERENCE: 210121.470C5

; CURRENT APPLICATION NUMBER: US/09/551,621

; CURRENT FILING DATE: 2000-04-17

; NUMBER OF SEQ ID NOS: 479

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 282

; LENGTH: 502

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-551-621-282

Query Match 100.0%; Score 21; DB 10; Length 502;

Best Local Similarity 100.0%; Pred. No. 0.95; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21

DB 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 8

US-10-007-805-282/c

; Sequence 282, Application US/10007805

; Publication No. US20020150581A1

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqin

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedavick, Thomas S.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Durham, Margareta

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.470C10

; CURRENT APPLICATION NUMBER: US/10/007,805

; CURRENT FILING DATE: 2001-12-07

; NUMBER OF SEQ ID NOS: 593

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 282

; LENGTH: 502

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-007-805-282

Query Match 100.0%; Score 21; DB 13; Length 502;

Best Local Similarity 100.0%; Pred. No. 0.95; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21

DB 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 9

US-10-076-622-282/c

; Sequence 282, Application US/10076622

; Publication No. US20030023036A1

; GENERAL INFORMATION:

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.470C11

; CURRENT APPLICATION NUMBER: US/10/076,622

; CURRENT FILING DATE: 2002-02-13

; NUMBER OF SEQ ID NOS: 627

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 282

; LENGTH: 502

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-076-622-282

Query Match 100.0%; Score 21; DB 14; Length 502;

Best Local Similarity 100.0%; Pred. No. 0.95; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21

DB 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 10

US-10-124-805-282/c

; Sequence 282, Application US/10124805

; Publication No. US20030166022A1

; GENERAL INFORMATION:

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.470C12

; CURRENT APPLICATION NUMBER: US/10/124,805

; CURRENT FILING DATE: 2002-04-15

; NUMBER OF SEQ ID NOS: 627

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 282

; LENGTH: 502

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-124-805-282

Query Match 100.0%; Score 21; DB 15; Length 502;

Best Local Similarity 100.0%; Pred. No. 0.95; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21

DB 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 11

US-10-097-340-74/c

; Sequence 74, Application US/10097340

; Publication No. US20030087250A1

; GENERAL INFORMATION:

```

; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VERIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-097-340-74

Query Match          100.0%; Score 21; DB 14; Length 1907;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTACCTCATGCGCCGGCTCAG 21
DB 1100 GTACCTCATGCGCCGGCTCAG 1080

RESULT 12
US-10-291-808-27/c
; Sequence 27, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
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; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-291-808-27
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Query Match          100.0%; Score 21; DB 15; Length 1907;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTACCTCATGCGCCGGCTCAG 21
DB 1100 GTACCTCATGCGCCGGCTCAG 1080
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RESULT 13
US-09-964-824A-101/c
; Sequence 101, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-964-824A-101

Query Match          100.0%; Score 21; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTACCTCATGCGCCGGCTCAG 21
DB 1124 GTACCTCATGCGCCGGCTCAG 1104
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RESULT 14
US-09-964-824A-563/c
; Sequence 563, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 563
; LENGTH: 1915
; TYPE: DNA
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ORGANISM: Homo sapiens
US-09-964-824A-563

Query Match 100.0%; Score 21; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCGGCTCAG 21
|||||
Db 1124 GTACCTCATGCGCGGCTCAG 1104

RESULT 15

US-09-880-107-3420/C
; Sequence 3420, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Schertf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3420
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843
US-09-880-107-3420

Query Match 100.0%; Score 21; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCGGCTCAG 21
|||||
Db 1124 GTACCTCATGCGCGGCTCAG 1104

Search completed: November 15, 2004, 23:08:56
Job time : 19.8491 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:35:22 ; Search time 1.77407 Seconds
(without alignments)
8413.757 Million cell updates/sec

Title: US-08-978-217-14

Sequence: 1 GTCACATGATGCGGCTCAG 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
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4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	237	4	US-09-016-434-927 Sequence 927, App
2	21	100.0	502	4	US-09-389-681-282 Sequence 282, App
3	21	100.0	502	4	US-09-620-405B-282 Sequence 282, App
4	21	100.0	502	4	US-09-339-338-282 Sequence 282, App
5	21	100.0	502	4	US-09-433-826B-282 Sequence 282, App
6	21	100.0	502	4	US-09-604-287A-282 Sequence 282, App
7	21	100.0	502	4	US-09-834-759-282 Sequence 282, App
8	21	100.0	502	4	US-09-590-751A-282 Sequence 282, App
9	21	100.0	1907	4	US-09-300-958A-27 Sequence 27, App
10	21	100.0	1907	4	US-09-570-593-4 Sequence 4, App
11	21	100.0	1920	1	US-08-746-789A-1 Sequence 1, App
12	16.4	78.1	1629	4	US-09-023-655-528 Sequence 528, App
13	16.4	78.1	2212	4	US-09-919-497-25 Sequence 1, App
14	16.4	78.1	5499	3	US-08-479-722B-1 Sequence 1, App
15	16.4	78.1	5499	3	US-08-592-685-1 Sequence 1, App
16	16.4	78.1	5502	2	PCT-US95-02251-17 Sequence 17, App
17	16.2	77.1	2266	2	US-08-213-767-1 Sequence 1, App
18	16.2	77.1	4403765	3	US-09-103-840A-2 Sequence 2, App
19	16.2	77.1	4403765	3	US-09-103-840A-2 Sequence 1, App
20	16.2	77.1	4411529	3	US-09-103-840A-1 Sequence 1, App
21	16.2	77.1	4411529	3	US-09-103-840A-1 Sequence 1, App
22	15.8	75.2	671	3	US-09-129-030-29 Sequence 29, App
23	15.8	75.2	1479	3	US-08-868-373-3 Sequence 3, App
24	15.8	75.2	1533	3	US-09-522-217-88 Sequence 88, App
25	15.8	75.2	1533	4	US-09-923-246-88 Sequence 88, App
26	15.8	75.2	1533	4	US-10-295-723-88 Sequence 88, App
27	15.8	75.2	2224	4	US-09-221-017B-384 Sequence 384, App

28	15.8	75.2	2877	4	US-09-619-353-1 Sequence 1, App
29	15.8	75.2	3072	3	US-09-522-217-55 Sequence 55, App
30	15.8	75.2	3072	4	US-09-923-246-55 Sequence 55, App
31	15.8	75.2	3072	4	US-10-295-723-55 Sequence 55, App
32	15.8	75.2	3072	4	US-09-825-561A-46 Sequence 46, App
33	15.4	73.3	1935	4	US-09-495-050A-190 Sequence 190, App
34	15.2	72.4	429	4	US-09-621-976-3360 Sequence 3260, App
35	15.2	72.4	848	3	US-09-009-913-338 Sequence 338, App
36	15.2	72.4	856	4	US-09-535-008-55 Sequence 55, App
37	15.2	72.4	1110	4	US-09-543-681A-3342 Sequence 3342, App
38	15.2	72.4	2218	4	US-09-350-457A-1 Sequence 1, App
39	15.2	72.4	2385	3	US-08-352-902D-145 Sequence 145, App
40	15.2	72.4	2484	2	US-08-209-521-8 Sequence 8, App
41	15.2	72.4	2484	3	US-08-961-810-4 Sequence 4, App
42	15.2	72.4	2484	3	US-08-352-902D-4 Sequence 4, App
43	15.2	72.4	2484	4	US-09-265-503B-4 Sequence 4, App
44	15.2	72.4	2484	4	US-09-708-200-16 Sequence 16, App
45	15.2	72.4	2484	4	US-09-788-657-10 Sequence 10, App

ALIGNMENTS

RESULT 1
US-09-016-434-927/c
Sequence 927, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESSES:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,021
REFERENCE/DOCKET NUMBER: PA-0002, US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 927:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNCR01
CLONE: 773734
US-09-016-434-927
Query Match 100.0%; Score 21; DB 4; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21
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Db 55 GTACCTCATGCGCCGGCTCAG 35

RESULT 2
US-09-389-681-282/c
; Sequence 282, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqin, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-389-681-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21
|||||
Db 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 3
US-09-620-4058-282/c
; Sequence 282, Application US/09620405B.
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqin
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-4058-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21
|||||
Db 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 4
US-09-339-338-282/c

; Sequence 282, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqin, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21
|||||
Db 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 5
US-09-433-826B-282/c
; Sequence 282, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqin
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-433-826B-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21
|||||
Db 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 6
US-09-604-287A-282/c
; Sequence 282, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqin
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND


```

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-282

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 502;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21
Db 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 7
US-09-834-759-282/c
; Sequence 282, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hedderston, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-282

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 502;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21
Db 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 8
US-09-590-751A-282/c
; Sequence 282, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C6
; CURRENT APPLICATION NUMBER: US/09/590,751A
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
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; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-751A-282

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 502;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21
Db 458 GTACCTCATGCGCCGGCTCAG 438

RESULT 9
US-09-300-958A-27/c
; Sequence 27, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-27

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 1907;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCCGGCTCAG 21
Db 1100 GTACCTCATGCGCCGGCTCAG 1080

RESULT 10
US-09-570-593-4/c
; Sequence 4, Application US/09570593
; Patent No. 6566063
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Harlowe, Greg
; TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
; FILE REFERENCE: 2300-1556
; CURRENT APPLICATION NUMBER: US/09/570,593
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
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LOCATION: (96)...(1211)
OTHER INFORMATION: Human epithelial-restricted with serine box (ESX)
OTHER INFORMATION: protein.
US-09-570-593-4

Query Match 100.0%; Score 21; DB 4; Length 1907;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCGGCTCAG 21
DB 1100 GTACCTCATGCGCGGCTCAG 1080

RESULT 11
US-08-746-789A-1/C
Sequence 1, Application US/08746789A
Patent No. 5789200

GENERAL INFORMATION:
APPLICANT: Ismail Kola, Martin J. Tyms, Christine Debouck
TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELF3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,789A
FILING DATE: No. 5789200ember 15, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG 50024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5219
TELEFAX: 610 270 4026
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1920
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No
US-08-746-789A-1

Query Match 100.0%; Score 21; DB 1; Length 1920;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTACCTCATGCGCGGCTCAG 21
DB 1119 GTACCTCATGCGCGGCTCAG 1099

RESULT 12
US-09-023-655-528/C
Sequence 528, Application US/09023655
Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023, 655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 528:
SEQUENCE CHARACTERISTICS:
LENGTH: 1629 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLNOT02
CLONE: 207681
US-09-023-655-528

Query Match 78.1%; Score 16.4; DB 4; Length 1629;
Best Local Similarity 94.4%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATGCGCGGCTCAG 21
DB 312 CCTCATGCGCGGCTCAG 295

RESULT 13
US-09-919-497-25/C
Sequence 25, Application US/09919497
Patent No. 6773883

GENERAL INFORMATION:
APPLICANT: Muller, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919, 497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221, 735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 2212
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Unsure
LOCATION: (625)...(625)
OTHER INFORMATION: n = a, c, g or t/u

US-09-919-497-25

Query Match 78.1%; Score 16.4; DB 4; Length 2212;
Best Local Similarity 94.4%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATGCGCCGGCTCAG 21
DB 884 CCTCTTGCGCCGGCTCAG 867

RESULT 14

US-08-479-722B-1/c
; Sequence 1, Application US/08479722B
; Patent No. 6074840
; GENERAL INFORMATION:
; APPLICANT: Bonadio, Jeffrey
; APPLICANT: Yin, Wushan
; TITLE OF INVENTION: LATENT TGF (BINDING PROTEIN (LTBP)
; TITLE OF INVENTION: GENES, COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Williams, Morgan & Amereson
; STREET: 7676 Hillmont, Suite 250
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77040
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,722B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US95/02251
; FILING DATE: 21-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/316,650
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/199,780
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fussey, Shelley P.M.
; REGISTRATION NUMBER: 39,458
; REFERENCE/DOCKET NUMBER: 4100.000500/FUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 934-7000
; TELEFAX: (713) 934-7011
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5499 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: /desc = "DNA"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..5499
; US-08-479-722B-1

Query Match 78.1%; Score 16.4; DB 3; Length 5499;
Best Local Similarity 94.4%; Pred. No. 78;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACCTCATGCGCCGGCTCA 20
DB 3158 ACCTCATGCGCCGGCTCA 3141

RESULT 15

US-09-592-685-1/c
; Sequence 1, Application US/09592685
; Patent No. 6774105
; GENERAL INFORMATION:
; APPLICANT: Bonadio, Jeffrey
; APPLICANT: Yin, Wushan
; TITLE OF INVENTION: LATENT TGF (BINDING PROTEIN (LTBP)
; TITLE OF INVENTION: GENES, COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Williams, Morgan & Amereson
; STREET: 7676 Hillmont, Suite 250
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77040
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/592,685
; FILING DATE: 12-JUN-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,722B
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US PCT/US95/02251
; FILING DATE: 21-FEB-1995
; APPLICATION NUMBER: US 08/316,650
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: US 08/199,780
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fussey, Shelley P.M.
; REGISTRATION NUMBER: 39,458
; REFERENCE/DOCKET NUMBER: 4100.000500/FUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 934-7000
; TELEFAX: (713) 934-7011
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5499 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: /desc = "DNA"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..5499
; US-09-592-685-1

Query Match 78.1%; Score 16.4; DB 4; Length 5499;
Best Local Similarity 94.4%; Pred. No. 78;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACCTCATGCGCCGGCTCA 20
DB 3158 ACCTCATGCGCCGGCTCA 3141

Search completed: November 15, 2004, 14:14:11
Job time : 10.7741 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:42:48 ; Search time 9.84905 Seconds
(without alignments)
11515.905 Million cell updates/sec

Title: US-08-978-217-13

Perfect score: 21
Sequence: 1 CCGGACATCTCATCCACC 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA:*

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- 2: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
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- 15: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	275	14	US-10-060-036-3261	Sequence 3261, App
2	100.0	499	9	US-09-998-598-2290	Sequence 2290, App
3	100.0	502	9	US-09-604-2874-282	Sequence 282, App
4	100.0	502	9	US-09-834-759-282	Sequence 282, App
5	100.0	502	9	US-09-339-338-282	Sequence 282, App
6	100.0	502	10	US-09-551-621-282	Sequence 282, App
7	100.0	502	13	US-10-007-805-282	Sequence 282, App
8	100.0	502	14	US-10-076-622-282	Sequence 282, App
9	100.0	502	15	US-10-124-805-282	Sequence 282, App
10	100.0	1435	15	US-10-017-161-1953	Sequence 1953, App
11	100.0	1435	15	US-10-292-798-1601	Sequence 1601, App
12	100.0	1907	14	US-10-097-340-74	Sequence 74, App1

13	100.0	1907	15	US-10-291-808-27	Sequence 27, App1
14	100.0	1915	9	US-09-964-824A-101	Sequence 101, App
15	100.0	1915	9	US-09-964-824A-563	Sequence 563, App
16	100.0	1915	9	US-09-880-107-3420	Sequence 3420, App
17	100.0	1915	9	US-09-967-768A-192	Sequence 192, App
18	100.0	1917	9	US-09-922-217-1105	Sequence 1105, App
19	100.0	1917	13	US-10-025-380-1105	Sequence 1105, App
20	100.0	1956	16	US-10-264-049-756	Sequence 756, App
21	100.0	1969	9	US-09-925-301-207	Sequence 207, App
22	100.0	2269	15	US-10-131-410-64	Sequence 64, App1
23	87.6	566	18	US-10-425-115-115220	Sequence 115220, App
24	84.8	450	9	US-09-864-761-21324	Sequence 21324, App
25	84.8	472	9	US-09-864-761-4580	Sequence 4580, App
26	80.0	471	10	US-09-918-995-23822	Sequence 23822, App
27	80.0	639	18	US-10-425-115-136062	Sequence 136062, App
28	80.0	792	13	US-10-027-632-138998	Sequence 138998, App
29	80.0	792	13	US-10-027-632-138998	Sequence 138998, App
30	80.0	792	15	US-10-027-632-138998	Sequence 138998, App
31	80.0	792	15	US-10-027-632-138998	Sequence 138998, App
32	80.0	825	15	US-10-369-493-43197	Sequence 43197, App
33	80.0	1321	16	US-10-425-114-3408	Sequence 3408, App
34	80.0	1604	16	US-10-425-114-33705	Sequence 33705, App
35	80.0	1626	16	US-10-156-761-4976	Sequence 4976, App
36	80.0	1635	17	US-10-437-963-10443	Sequence 10443, App
37	80.0	1702	18	US-10-425-115-20976	Sequence 20976, App
38	80.0	2283	17	US-10-767-701-13528	Sequence 13528, App
39	80.0	2297	16	US-10-425-114-10844	Sequence 10844, App
40	80.0	2497	16	US-10-425-114-33345	Sequence 33345, App
41	80.0	2539	14	US-10-198-846-13456	Sequence 13456, App
42	80.0	3049	15	US-10-120-988-186	Sequence 186, App
43	80.0	3083	16	US-10-138-588-21	Sequence 21, App1
44	80.0	9025608	15	US-10-156-761-1	Sequence 1, App1
45	78.1	25	16	US-10-161-493-166	Sequence 166, App

ALIGNMENTS

RESULT 1
US-10-060-036-3261
; Sequence 3261, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Peters, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugui
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060, 036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3261
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3261

Query Match 100.0%; Score 21; DB 14; Length 275;
Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0

Qy 1 CCGGACATCTCATCCACC 21
Db 109 CCGGACATCTCATCCACC 129

RESULT 2
US-09-998-598-2290/c

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/ Sequence 2290, Application US/0998598
/ Patent No. US20020150922A1
/ GENERAL INFORMATION:
/ APPLICANT: Stolk, John A.
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Chenault, Ruth A.
/ APPLICANT: Meagher, Madelein Joy
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
/ FILE REFERENCE: 210121.561
/ CURRENT APPLICATION NUMBER: US/09/998,598
/ CURRENT FILING DATE: 2001-11-16
/ NUMBER OF SEQ ID NOS: 2606
/ SOFTWARE: Corixa Invention Disclosure Database
/ SEQ ID NO 2290
/ LENGTH: 499
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-998-598-2290
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Query Match 100.0%; Score 21; DB 9; Length 499;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCGGACATCTCTCATCCACC 21
DB 324 CCGGACATCTCTCATCCACC 304
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RESULT 3
US-09-604-287A-282
/ Sequence 282, Application US/09604287A
/ Patent No. US20020064872A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Yugui
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Hepler, William T.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
/ FILE REFERENCE: 210121.470C7
/ CURRENT APPLICATION NUMBER: US/09/604,287A
/ CURRENT FILING DATE: 2000-06-22
/ NUMBER OF SEQ ID NOS: 489
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 282
/ LENGTH: 502
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-604-287A-282
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Query Match 100.0%; Score 21; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCGGACATCTCTCATCCACC 21
DB 290 CCGGACATCTCTCATCCACC 310
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RESULT 4
US-09-834-759-282
/ Sequence 282, Application US/09834759
/ Publication No. US20020085998A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Yugui
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Hepler, William T.
```

```
/ APPLICANT: Henderson, Robert A.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
/ FILE REFERENCE: 210121.470C9
/ CURRENT APPLICATION NUMBER: US/09/834,759
/ CURRENT FILING DATE: 2001-04-13
/ NUMBER OF SEQ ID NOS: 547
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 282
/ LENGTH: 502
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-834-759-282
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Query Match 100.0%; Score 21; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCGGACATCTCTCATCCACC 21
DB 290 CCGGACATCTCTCATCCACC 310
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RESULT 5
US-09-339-338-282
/ Sequence 282, Application US/09339338A
/ Patent No. US20020102602A1
/ GENERAL INFORMATION:
/ APPLICANT: Yugui, Jiang
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Xu, Jiangchun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
/ TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.470C2
/ CURRENT APPLICATION NUMBER: US/09/339,338A
/ CURRENT FILING DATE: 1999-06-23
/ NUMBER OF SEQ ID NOS: 315
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 282
/ LENGTH: 502
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-339-338-282
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Query Match 100.0%; Score 21; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCGGACATCTCTCATCCACC 21
DB 290 CCGGACATCTCTCATCCACC 310
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RESULT 6
US-09-551-621-282
/ Sequence 282, Application US/09551621
/ Publication No. US20030104366A1
/ GENERAL INFORMATION:
/ APPLICANT: Yugui, Jiang
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Harlocker, Susan L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
/ TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.470C5
/ CURRENT APPLICATION NUMBER: US/09/551,621
/ CURRENT FILING DATE: 2000-04-17
/ NUMBER OF SEQ ID NOS: 479
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 282
/ LENGTH: 502
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-551-621-282

Query Match 100.0%; Score 21; DB 10; Length 502;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
Db 290 CCGGACATCTCATCCACC 310

RESULT 7

US-10-007-805-282
Sequence 282, Application US/10007805
Publication No. US20020150581A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C10
CURRENT APPLICATION NUMBER: US/10/007,805
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 593
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-10-007-805-282

Query Match 100.0%; Score 21; DB 13; Length 502;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
Db 290 CCGGACATCTCATCCACC 310

RESULT 8

US-10-076-622-282
Sequence 282, Application US/10076622
Publication No. US2003023036A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C11
CURRENT APPLICATION NUMBER: US/10/076,622
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 627
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-10-076-622-282

Query Match 100.0%; Score 21; DB 14; Length 502;

Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
Db 290 CCGGACATCTCATCCACC 310

RESULT 9

US-10-124-805-282
Sequence 282, Application US/10124805
Publication No. US2003016602A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C12
CURRENT APPLICATION NUMBER: US/10/124,805
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 627
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-10-124-805-282

Query Match 100.0%; Score 21; DB 15; Length 502;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
Db 290 CCGGACATCTCATCCACC 310

RESULT 10

US-10-017-161-1953/C
Sequence 1953, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 08435/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1953
LENGTH: 1435
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: source
LOCATION: (1)..(1435)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(1235)
FEATURE:
NAME/KEY: modified_base
LOCATION: (1040)..(1139)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (1145)
OTHER INFORMATION: a, t, c, g, unknown or other

US-10-017-161-1953

Query Match 100.0%; Score 21; DB 15; Length 1435;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
DB 335 CCGGACATCTCATCCACC 315

RESULT 11

US-10-292-798-1601/c
; Sequence 1601, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: AURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1601
; LENGTH: 1435
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1435)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1235)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1040)..(1139)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (1145)..(1145)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-292-798-1601

Query Match 100.0%; Score 21; DB 15; Length 1435;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
DB 335 CCGGACATCTCATCCACC 315

RESULT 12

US-10-097-340-74
; Sequence 74, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATYAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT

; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BASF, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO

; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-74

Query Match 100.0%; Score 21; DB 14; Length 1907;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
DB 932 CCGGACATCTCATCCACC 952

RESULT 13

US-10-291-808-27
; Sequence 27, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-291-808-27

Query Match 100.0%; Score 21; DB 15; Length 1907;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21
Db 932 CCGGACATCCTCATCCACC 952

Db 956 CCGGACATCCTCATCCACC 976

Search completed: November 15, 2004, 23:08:46
Job time: 14.8491 secs

RESULT 14
US-09-964-824A-101

; Sequence 101, Application US/09964824A
; Patent No. US20020102531A1

; GENERAL INFORMATION:

; APPLICANT: Horrigan, Stephen

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

; FILE REFERENCE: 689290-73

; CURRENT APPLICATION NUMBER: US/09/964,824A

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US/60/236,033

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236,032

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236,028

; PRIOR FILING DATE: 2000-09-28

; NUMBER OF SEQ ID NOS: 583

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 101

; LENGTH: 1915

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-964-824A-101

Query Match 100.0%; Score 21; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21
Db 956 CCGGACATCCTCATCCACC 976

RESULT 15
US-09-964-824A-563

; Sequence 563, Application US/09964824A
; Patent No. US20020102531A1

; GENERAL INFORMATION:

; APPLICANT: Horrigan, Stephen

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

; FILE REFERENCE: 689290-73

; CURRENT APPLICATION NUMBER: US/09/964,824A

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US/60/236,033

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236,032

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236,028

; PRIOR FILING DATE: 2000-09-28

; NUMBER OF SEQ ID NOS: 583

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 563

; LENGTH: 1915

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-964-824A-563

Query Match 100.0%; Score 21; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:35:22 ; Search time 1.77407 Seconds
(without alignments)
8413.757 Million cell updates/sec

Title: US-08-978-217-13

Perfect score: 21

Sequence: 1 CCGGACATCCATCCATCCACC 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	502	4 US-09-389-681-282	Sequence 282, App
2	21	100.0	502	4 US-09-620-405B-282	Sequence 282, App
3	21	100.0	502	4 US-09-339-338-282	Sequence 282, App
4	21	100.0	502	4 US-09-433-826B-282	Sequence 282, App
5	21	100.0	502	4 US-09-604-287A-282	Sequence 282, App
6	21	100.0	502	4 US-09-834-759-282	Sequence 282, App
7	21	100.0	502	4 US-09-590-751A-282	Sequence 282, App
8	21	100.0	1907	4 US-09-300-958A-27	Sequence 27, App1
9	21	100.0	1907	4 US-09-570-593-4	Sequence 4, App1
10	21	100.0	1920	4 US-08-746-789A-1	Sequence 1, App1
11	16.8	80.0	3049	4 US-09-774-528-186	Sequence 186, App1
12	16.4	78.1	1086	4 US-09-328-352-99	Sequence 99, App1
13	16.4	78.1	3346	4 US-09-684-405-5	Sequence 5, App1
14	16.2	77.1	165	1 US-08-456-647B-1	Sequence 1, App1
15	16.2	77.1	165	1 US-08-237-401A-1	Sequence 1, App1
16	16.2	77.1	361	4 US-09-643-597-303	Sequence 303, App
17	16.2	77.1	361	4 US-09-480-884A-303	Sequence 303, App
18	16.2	77.1	361	4 US-09-542-615A-303	Sequence 303, App
19	16.2	77.1	361	4 US-09-606-421B-303	Sequence 303, App
20	16.2	77.1	361	4 US-09-630-940B-303	Sequence 303, App
21	16.2	77.1	427	3 US-09-328-111-567	Sequence 567, App
22	16.2	77.1	1002	4 US-09-540-236-849	Sequence 849, App
23	16.2	77.1	1195	4 US-09-270-767-13861	Sequence 13861, A
24	16.2	77.1	1223	4 US-09-814-915A-89	Sequence 89, App1
25	16.2	77.1	1228	3 US-08-826-246-9	Sequence 9, App1
26	16.2	77.1	1228	3 US-08-944-495-9	Sequence 9, App1
27	16.2	77.1	1228	3 US-09-126-640-5	Sequence 5, App1

C 28	16.2	77.1	1228	3 US-08-925-588-9	Sequence 9, App1
C 29	16.2	77.1	1228	4 US-09-288-292A-5	Sequence 5, App1
C 30	16.2	77.1	1228	4 US-09-372-044-9	Sequence 9, App1
C 31	16.2	77.1	1228	4 US-08-825-486-9	Sequence 9, App1
C 32	16.2	77.1	1228	4 US-08-826-246-9	Sequence 9, App1
C 33	16.2	77.1	1228	4 US-09-614-912-139	Sequence 139, App
C 34	16.2	77.1	16891	4 US-09-486-147-1	Sequence 1, App1
C 35	15.8	75.2	718	3 US-08-998-416-682	Sequence 682, App
C 36	15.8	75.2	1362	4 US-09-252-991A-10470	Sequence 10470, A
C 37	15.8	75.2	1826	4 US-09-252-991A-10598	Sequence 10598, A
C 38	15.8	75.2	1884	4 US-09-620-312D-287	Sequence 287, App
C 39	15.8	75.2	2190	4 US-09-252-991A-10256	Sequence 10256, A
C 40	15.4	73.3	1509	4 US-09-248-796A-4401	Sequence 4401, Ap
C 41	15.2	72.4	464	4 US-09-513-998C-889	Sequence 889, App
C 42	15.2	72.4	492	4 US-09-252-991A-880	Sequence 880, App
C 43	15.2	72.4	510	4 US-09-252-991A-4285	Sequence 4285, Ap
C 44	15.2	72.4	562	4 US-09-621-976-1319	Sequence 1319, Ap
C 45	15.2	72.4	636	4 US-09-702-705-1668	Sequence 1668, Ap

ALIGNMENTS

```
RESULT 1
US-09-389-681-282
; Sequence 282, Application US/09389681A-
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqin, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.47003
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-389-681-282

Query Match      100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCCATCCATCCACC 21
DB 290 CCGGACATCCATCCATCCACC 310

RESULT 2
US-09-620-405B-282
; Sequence 282, Application US/09620405B-
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.47008
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
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LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-09-620-4058-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21
DB 290 CCGGACATCCTCATCCACC 310

RESULT 3
US-09-339-338-282
Sequence 282, Application US/09339338A

PATENT No. 6573368
GENERAL INFORMATION:
APPLICANT: Yugu, JIANG
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, JIANGCHUN
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
FILE REFERENCE: 210121.470C2
CURRENT APPLICATION NUMBER: US/09/339,338A
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ. ID NOS: 315
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-09-339-338-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21
DB 290 CCGGACATCCTCATCCACC 310

RESULT 4
US-09-433-826B-282
Sequence 282, Application US/09433826B

PATENT No. 6579973
GENERAL INFORMATION:
APPLICANT: JIANG, YUGU
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, JIANGCHUN
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
FILE REFERENCE: 210121.470C4
CURRENT APPLICATION NUMBER: US/09/433,826B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ. ID NOS: 474
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-09-433-826B-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21

DB 290 CCGGACATCCTCATCCACC 310

RESULT 5
US-09-604-287A-282
Sequence 282, Application US/09604287A

PATENT No. 6586572
GENERAL INFORMATION:
APPLICANT: JIANG, YUGU
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, JIANGCHUN
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ. ID NOS: 489
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-09-604-287A-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21
DB 290 CCGGACATCCTCATCCACC 310

RESULT 6
US-09-834-759-282
Sequence 282, Application US/09834759

PATENT No. 6680197
GENERAL INFORMATION:
APPLICANT: JIANG, YUGU
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, JIANGCHUN
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ. ID NOS: 547
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 282
LENGTH: 502
TYPE: DNA
ORGANISM: Homo sapiens
US-09-834-759-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21
DB 290 CCGGACATCCTCATCCACC 310

RESULT 7
US-09-590-751A-282

; Sequence 282, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
; FILE REFERENCE: 210121.47006
; CURRENT APPLICATION NUMBER: US/09/590.751A
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-751A-282

Query Match 100.0%; Score 21; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
DB 290 CCGGACATCTCATCCACC 310

RESULT 8

US-09-300-958A-27
; Sequence 27, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300.958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083.331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098.070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118.624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-27

Query Match 100.0%; Score 21; DB 4; Length 1907;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
DB 932 CCGGACATCTCATCCACC 952

RESULT 9

US-09-570-593-4
; Sequence 4, Application US/09570593
; Patent No. 6566063
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong

; APPLICANT: Harrowe, Greg
; TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
; FILE REFERENCE: 2300-1556
; CURRENT APPLICATION NUMBER: US/09/570.593
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134.112
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1211)
; OTHER INFORMATION: Human epithelial-restricted with serine box (ESX)
; OTHER INFORMATION: protein.
US-09-570-593-4

Query Match 100.0%; Score 21; DB 4; Length 1907;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
DB 932 CCGGACATCTCATCCACC 952

RESULT 10

US-08-746-789A-1
; Sequence 1, Application US/08746789A
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismail Kola, Martin J. Tyms, Christine DeBouck
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELP3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746.789A
; FILING DATE: No. 5789200el October 15, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG 50024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5219
; TELEFAX: 610 270 4026
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-08-746-789A-1

Query Match 100.0%; Score 21; DB 1; Length 1920;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 21
DB 951 CCGGACATCTCATCCACC 971

RESULT 11

US-09-774-528-186/c
; Sequence 186, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrul
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ. ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 186
; LENGTH: 3049
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21)..(3002)
US-09-774-528-186

Query Match 80.0%; Score 16.8; DB 4; Length 3049;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGGACATCTCATCCACC 20
DB 726 CCGGACATCTCATCCACC 707

RESULT 12

US-09-328-352-99/c
; Sequence 99, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ. ID NOS: 8252
; SEQ ID NO 99
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-99

Query Match 78.1%; Score 16.4; DB 4; Length 1086;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGACATCTCATCCACC 21
DB 75 GGACATCTCATCCACC 58

RESULT 13

US-09-684-405-5/c
; Sequence 5, Application US/09684405
; Patent No. 6770477
; GENERAL INFORMATION:
; APPLICANT: Dennis J. Slamon
; APPLICANT: Juliana J. Oh
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES
; TITLE OF INVENTION: ASSOCIATED WITH HER-2/NEU OVEREXPRESSION
; FILE REFERENCE: 30448, 79USU1
; CURRENT APPLICATION NUMBER: US/09/684,405
; CURRENT FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/157,923
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ. ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3346
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-684-405-5

Query Match 78.1%; Score 16.4; DB 4; Length 3346;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGACATCTCATCCACC 21
DB 3224 GGACATCTCATCCACC 3207

RESULT 14

US-08-456-647B-1/c
; Sequence 1, Application US/08456647B
; Patent No. 5811516
; GENERAL INFORMATION:
; APPLICANT: Lemke Ph.D. et al., Greg E.
; TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,647B
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/237,401
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/884,486
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07251/007002
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
CLONE: Tyro-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..165
US-08-456-647B-1

Query Match 77.1%; Score 16.2; DB 1; Length 165;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21
Db 76 CCGGATCATCTCAAGCACCC 56

RESULT 15

US-08-237-401A-1/C
Sequence 1, Application US/08237401A
Patent No. 5837448
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
CLONE: Tyro-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..165
US-08-237-401A-1

Query Match 77.1%; Score 16.2; DB 2; Length 165;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCGGACATCCTCATCCACC 21
Db 76 CCGGATCATCTCAAGCACCC 56

Search completed: November 15, 2004, 14:14:02
Job time: 2.77407 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 21:57:02 ; Search time 26.9264 Seconds
(without alignments)

3209.338 Million cell updates/sec

Title: US-08-978-217-12

Perfect score: 84
Sequence: 1 KNSGKMKKEEVVQSRN 16

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -OFAST=fastap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human0.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0
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-FEAROP=6 -FEAREXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

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11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
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13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	237	16 US-10-305-720-927	Sequence 927, App
2	84	100.0	451	9 US-09-998-598-32	Sequence 32, App1
3	84	100.0	463	15 US-10-281-808-25	Sequence 25, App1
4	84	100.0	499	9 US-09-998-598-2290	Sequence 2290, App
5	84	100.0	528	14 US-10-066-543-3233	Sequence 3233, App
6	84	100.0	620	14 US-10-060-036-2379	Sequence 2379, App
7	84	100.0	1907	14 US-10-097-340-74	Sequence 74, App1
8	84	100.0	1907	15 US-10-291-808-27	Sequence 27, App1
9	84	100.0	1915	9 US-09-964-824A-101	Sequence 101, App
10	84	100.0	1915	9 US-09-964-824A-563	Sequence 563, App
11	84	100.0	1915	9 US-09-880-107-3420	Sequence 3420, App
12	84	100.0	1915	9 US-09-967-768A-192	Sequence 192, App
13	84	100.0	1917	9 US-09-922-217-1105	Sequence 1105, App
14	84	100.0	1917	13 US-10-025-880-1105	Sequence 1105, App
15	84	100.0	1956	16 US-10-264-049-156	Sequence 756, App
16	84	100.0	1996	9 US-09-925-301-207	Sequence 207, App1
17	84	100.0	2269	15 US-10-131-410-64	Sequence 64, App1
18	57	67.9	1601	16 US-09-986-480-40	Sequence 40, App1
19	52	61.9	1601	16 US-10-062-674-1730	Sequence 1730, App
20	50	59.5	535	15 US-10-029-386-3052	Sequence 3052, App
21	50	59.5	11788	15 US-10-316-253-263	Sequence 263, App1
22	50	59.5	11788	16 US-10-205-331-3	Sequence 3, App1
23	50	59.5	11788	17 US-10-311-527-3	Sequence 3, App1
24	50	59.5	235070	13 US-10-087-192-1990	Sequence 1990, App
25	49	58.3	807	13 US-10-027-632-167020	Sequence 167020, App
26	49	58.3	807	15 US-10-027-632-167020	Sequence 167020, App
27	48	57.1	174	9 US-09-933-797-678	Sequence 678, App
28	48	57.1	1642	16 US-10-424-599-30786	Sequence 30786, App
29	48	57.1	2046	16 US-10-425-115-95484	Sequence 95484, App
30	48	57.1	36048	16 US-10-052-482-127	Sequence 127, App
31	47	56.0	402	10 US-09-918-995-33421	Sequence 33421, App
32	47	56.0	2498	16 US-10-424-599-30786	Sequence 130502, App
33	47	56.0	254366	16 US-09-822-871-3	Sequence 3, App1
34	47	56.0	254366	16 US-10-673-885-3	Sequence 3, App1
35	47	56.0	374849	13 US-10-087-192-1627	Sequence 1627, App
36	46.5	55.4	787	13 US-10-027-632-125191	Sequence 125191, App
37	46.5	55.4	787	15 US-10-027-632-125191	Sequence 125191, App
38	46	54.8	495	16 US-10-424-599-89196	Sequence 89196, App
39	46	54.8	552	13 US-10-027-632-90917	Sequence 90917, App
40	46	54.8	552	15 US-10-027-632-90917	Sequence 90917, App
41	46	54.8	1035	16 US-10-282-122A-15940	Sequence 15940, App
42	46	54.8	1571	9 US-09-938-842A-4493	Sequence 4493, App
43	46	54.8	1571	11 US-09-938-842A-4493	Sequence 4493, App
44	46	54.8	2294	16 US-10-425-114-32979	Sequence 32979, App
45	46	54.8	3060	9 US-09-938-842A-760	Sequence 760, App

ALIGNMENTS

RESULT 1
US-10-305-720-927
; Sequence 927, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 927
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040010136A1 773734

APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Indira, Carol Yoseph
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Carter, Derrick
APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carole L.
APPLICANT: Durham, Margarita
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3233
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 438
OTHER INFORMATION: n = A,T,C or G
US-10-066-543-3233

Alignment Scores:
Pred. No.: 1.16e-05 Length: 528
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-08-978-217-12 (1-16) x US-10-066-543-3233 (1-528)

QY 1 LysAenSerGlyTrpLysGluGluValLeuGlnSerArgAsn 16
DB 63 AAAAAGCTCAAGCGGCTGGAAGAGAGAGGTTCTCCAGAGTCGGAAC 110

RESULT 6
US-10-060-036-2379
Sequence 2379, Application US/10060036
Publication No. US2003007314A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yugu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2379
LENGTH: 620
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 169, 456, 487, 488, 602
OTHER INFORMATION: n = A,T,C or G
US-10-060-036-2379

Alignment Scores:
Pred. No.: 1.38e-05 Length: 620
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-08-978-217-12 (1-16) x US-10-060-036-2379 (1-620)

QY 1 LysAenSerGlyTrpLysGluGluValLeuGlnSerArgAsn 16
DB 63 AAAAAGCTCAAGCGGCTGGAAGAGAGAGGTTCTCCAGAGTCGGAAC 110

RESULT 7
US-10-097-340-74
Sequence 74, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, JR.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
FILE REFERENCE: MRI-030 Assessment, Prevention, and Therapy of Ovarian Cancer
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 74
LENGTH: 1907
TYPE: DNA
ORGANISM: Homo sapiens
US-10-097-340-74

Alignment Scores:
Pred. No.: 4.58e-05 Length: 1907
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-08-978-217-12 (1-16) x US-10-097-340-74 (1-1907)

QY 1 LysAenSerGlyTrpLysGluGluValLeuGlnSerArgAsn 16
DB 1161 AAAAAGCTCAAGCGGCTGGAAGAGAGAGGTTCTCCAGAGTCGGAAC 1208
RESULT 8

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US-10-291-808-27
; Sequence 27, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-291-808-27

Alignment Scores:
Pred. No.: 4.58e-05 Length: 1907
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-08-978-217-12 (1-16) x US-10-291-808-27 (1-1907)
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Db 1161 AAAAAGCTCAAGCGGCTGGAGAGAGAGAGAGAGGTTCTCCAGAGTCGGAAC 1208

RESULT 9
US-09-964-824A-101
; Sequence 101, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 101
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-101

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Pred. No.: 4.6e-05 Length: 1915
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB: 9 Gaps: 0
US-08-978-217-12 (1-16) x US-09-964-824A-101 (1-1915)
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Db 1185 AAAAAGCTCAAGCGGCTGGAGAGAGAGAGAGGTTCTCCAGAGTCGGAAC 1232

RESULT 10
US-09-964-824A-563
; Sequence 563, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 563
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-563

Alignment Scores:
Pred. No.: 4.6e-05 Length: 1915
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-978-217-12 (1-16) x US-09-964-824A-563 (1-1915)
Qy 1 LysAsnSerSerGlyTrrpLysGluGluValLeuGlnSerArgAsn 16
Db 1185 AAAAAGCTCAAGCGGCTGGAGAGAGAGAGAGGTTCTCCAGAGTCGGAAC 1232

RESULT 11
US-09-880-107-3420
; Sequence 3420, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3420
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843
US-09-880-107-3420
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Alignment Scores:
Pred. No.: 4,6e-05 Length: 1915
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-08-978-217-12 (1-16) x US-09-880-107-3420 (1-1915)

Qy 1 LysAenSerGlyTTrpLysGluGluValLeuGlnSerArgAsn 16
Db 1185 AAAAAGCTCAAGCGGCTGGAAGAGGAGGTTCTCCAGAGTCGGAAC 1232

RESULT 12
US-09-967-768A-192
Sequence 192, Application US/09967768A
Patent No. US20020150877A1
GENERAL INFORMATION:
APPLICANT: Anguereus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: Patentin version 3.0
SEQ ID NO 192
LENGTH: 1915
TYPE: DNA
ORGANISM: Homo sapiens
US-09-967-768A-192

Alignment Scores:
Pred. No.: 4,6e-05 Length: 1915
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-08-978-217-12 (1-16) x US-09-967-768A-192 (1-1915)

Qy 1 LysAenSerGlyTTrpLysGluGluValLeuGlnSerArgAsn 16
Db 1185 AAAAAGCTCAAGCGGCTGGAAGAGGAGGTTCTCCAGAGTCGGAAC 1232

RESULT 13
US-09-922-217-1105
Sequence 1105, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secretist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yudi
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1105
LENGTH: 1917
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-217-1105

Alignment Scores:
Pred. No.: 4,61e-05 Length: 1917
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-08-978-217-12 (1-16) x US-09-922-217-1105 (1-1917)

Qy 1 LysAenSerGlyTTrpLysGluGluValLeuGlnSerArgAsn 16
Db 1187 AAAAAGCTCAAGCGGCTGGAAGAGGAGGTTCTCCAGAGTCGGAAC 1234

RESULT 14
US-10-025-380-1105
Sequence 1105, Application US/10025380
Publication No. US20020182191A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secretist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yudi
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Gary A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1105
LENGTH: 1917
TYPE: DNA
ORGANISM: Homo sapiens
US-10-025-380-1105

Alignment Scores:
Pred. No.: 4,61e-05 Length: 1917
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-08-978-217-12 (1-16) x US-10-025-380-1105 (1-1917)

Qy 1 LysAenSerGlyTTrpLysGluGluValLeuGlnSerArgAsn 16
Db 1187 AAAAAGCTCAAGCGGCTGGAAGAGGAGGTTCTCCAGAGTCGGAAC 1234

RESULT 15
US-10-264-049-756
; Sequence 756, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Btze et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antipodles
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 756
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-049-756

Alignment Scores:
Pred. No.: 4.71e-05 Length: 1956
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-08-978-217-12 (1-16) x US-10-264-049-756 (1-1956)

OY 1 LysAsnSerSerGlyTyrPlySGluGluValLeuGlnSerArgAsn 16
1226 AAAAAGCTCAAGCGCTGGAAGGAGGAAGAGTCTCCAGAGTCGAAC 1273

Search completed: November 16, 2004, 03:19:05
Job time : 35.4264 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 14:00:59 ; Search time 4.94062 Seconds
(without alignments)
2301.862 Million cell updates/sec

Title: US-08-978-217-12

Perfect score: 84
Sequence: 1 KNSGCKKEEVLQSRN 16

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPPO_spool_p/US08978217/runat.15112004.103131.12764/app_query.fasta_1.1500
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=xrni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptio -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08978217@cgn2_1.1.213@runat.15112004.103131.12764 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOBQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfillseq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	237	4	US-09-016-434-927 Sequence 927, App
2	84	100.0	463	4	US-09-300-958A-25 Sequence 25, Appl
3	84	100.0	1907	4	US-09-300-958A-27 Sequence 27, Appl
4	84	100.0	1907	4	US-09-570-593-4 Sequence 4, Appl
5	84	100.0	1920	4	US-08-746-789A-1 Sequence 1, Appl
6	47	56.0	2719	4	US-09-976-594-959 Sequence 959, App
7	47	56.0	254366	4	US-09-822-871-3 Sequence 3, Appl
8	46	54.8	1348	4	US-09-638-649-6 Sequence 6, Appl
9	46	54.8	8100	4	US-09-554-337-4 Sequence 4, Appl
10	46	54.8	11517	3	US-07-920-281C-1 Sequence 1, Appl
11	46	54.8	11517	3	US-08-466-277-1 Sequence 1, Appl
12	46	54.8	11517	4	US-09-688-842-1 Sequence 1, Appl

13	46	54.8	15538	4	US-09-554-337-1	Sequence 1, Appl
14	45	53.6	993	4	US-09-464-535-25	Sequence 25, Appl
15	45	53.6	7492	4	US-09-299-141-5	Sequence 5, Appl
16	45	53.6	10627	1	US-08-060-925A-12	Sequence 12, Appl
17	45	53.6	12222	4	US-09-328-975-42	Sequence 42, Appl
18	44	52.4	2763	4	US-09-668-680-8	Sequence 8, Appl
19	44	52.4	3396	4	US-09-668-680-6	Sequence 6, Appl
20	44	52.4	3423	4	US-09-668-680-7	Sequence 7, Appl
21	44	52.4	50000	3	US-09-146-053-4	Sequence 4, Appl
22	44	52.4	640681	4	US-09-790-988-1	Sequence 1, Appl
23	43	51.2	517	4	US-09-621-976-10337	Sequence 10337, A
24	43	51.2	4417	3	US-07-741-453A-57	Sequence 57, Appl
25	43	51.2	8543	3	US-08-496-944-1	Sequence 1, Appl
26	42.5	50.6	6396	4	US-09-620-312D-226	Sequence 226, App
27	42	50.0	244	4	US-09-513-999C-11811	Sequence 11811, A
28	42	50.0	546	4	US-09-248-796A-1499	Sequence 1499, Ap
29	42	50.0	694	2	US-08-537-400-15	Sequence 15, Appl
30	42	50.0	694	2	US-08-706-702-17	Sequence 17, Appl
31	42	50.0	694	4	US-08-706-706-17	Sequence 17, Appl
32	42	50.0	694	4	US-09-238-471-17	Sequence 17, Appl
33	42	50.0	1265	4	US-09-702-705-95	Sequence 95, Appl
34	42	50.0	1265	4	US-09-736-457-95	Sequence 95, Appl
35	42	50.0	1265	4	US-09-614-124B-95	Sequence 95, Appl
36	42	50.0	1265	4	US-09-671-325-95	Sequence 95, Appl
37	42	50.0	1265	4	US-09-589-184-95	Sequence 95, Appl
38	42	50.0	1265	4	US-09-658-824-95	Sequence 95, Appl
39	42	50.0	1383	4	US-09-270-767-21657	Sequence 6375, Ap
40	42	50.0	1383	4	US-08-484-661A-38	Sequence 21657, A
41	42	50.0	1485	3	US-08-484-661A-38	Sequence 38, Appl
42	42	50.0	1485	3	US-08-656-664-38	Sequence 38, Appl
43	42	50.0	1485	5	PCT-US96-09641-38	Sequence 38, Appl
44	42	50.0	1575	4	US-09-248-796A-4522	Sequence 4522, Ap
45	42	50.0	1716	3	US-08-484-661A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-016-434-927
Sequence 927, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF SEQUENCES: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555

```

/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 927:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 237 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: COLNCR01
/ CLONE: 773734
US-09-016-434-927

Alignment Scores:
Pred. No.: 1.76e-06 Length: 237
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-08-978-217-12 (1-16) x US-09-016-434-927 (1-237)

QY 1 LysAenSerSerGlyTrrpLysGluGluValLeuGlnSerArgAsn 16
Db 116 AAAAAGCTCAAGCGGCTGGAAGAGAGAGAGGTTCTCCAGTGGAGAC 163

RESULT 2
US-09-300-958A-25
/ Sequence 25, Application US/09300958A
/ Patent No. 6495319
/ GENERAL INFORMATION:
/ APPLICANT: McClelland, Michael
/ APPLICANT: Welsh, John
/ APPLICANT: Trenkle, Thomas
/ TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
/ FILE REFERENCE: P-PH 3457
/ CURRENT APPLICATION NUMBER: US/09/300,958A
/ CURRENT FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: 60/083,331
/ PRIOR FILING DATE: 1998-04-27
/ PRIOR APPLICATION NUMBER: 60/098,070
/ PRIOR FILING DATE: 1998-08-27
/ PRIOR APPLICATION NUMBER: 60/118,624
/ PRIOR FILING DATE: 1999-02-04
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 25
/ LENGTH: 463
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (368)
/ NAME/KEY: unsure
/ LOCATION: (402)
/ NAME/KEY: unsure
/ LOCATION: (458)
US-09-300-958A-25

Alignment Scores:
Pred. No.: 3.9e-06 Length: 463
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-08-978-217-12 (1-16) x US-09-300-958A-25 (1-463)

QY 1 LysAenSerSerGlyTrrpLysGluGluValLeuGlnSerArgAsn 16
Db 8 AAAAAGCTCAAGCGGCTGGAAGAGAGAGAGGTTCTCCAGTGGAGAC 55
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RESULT 3
US-09-300-958A-27
/ Sequence 27, Application US/09300958A
/ Patent No. 6495319
/ GENERAL INFORMATION:
/ APPLICANT: McClelland, Michael
/ APPLICANT: Welsh, John
/ APPLICANT: Trenkle, Thomas
/ TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
/ FILE REFERENCE: P-PH 3457
/ CURRENT APPLICATION NUMBER: US/09/300,958A
/ CURRENT FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: 60/083,331
/ PRIOR FILING DATE: 1998-04-27
/ PRIOR APPLICATION NUMBER: 60/098,070
/ PRIOR FILING DATE: 1998-08-27
/ PRIOR APPLICATION NUMBER: 60/118,624
/ PRIOR FILING DATE: 1999-02-04
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 27
/ LENGTH: 1907
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-300-958A-27

Alignment Scores:
Pred. No.: 2.1e-05 Length: 1907
Score: 84.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-08-978-217-12 (1-16) x US-09-300-958A-27 (1-1907)

QY 1 LysAenSerSerGlyTrrpLysGluGluValLeuGlnSerArgAsn 16
Db 1161 AAAAAGCTCAAGCGGCTGGAAGAGAGAGAGGTTCTCCAGTGGAGAC 1208

RESULT 4
US-09-570-593-4
/ Sequence 4, Application US/09570593
/ Patent No. 6566063
/ GENERAL INFORMATION:
/ APPLICANT: Kaufmann, Joerg
/ APPLICANT: Xin, Hong
/ APPLICANT: Hartowe, Greg
/ TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
/ FILE REFERENCE: 2300-1556
/ CURRENT APPLICATION NUMBER: US/09/570,593
/ CURRENT FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: 60/134,112
/ PRIOR FILING DATE: 1999-05-14
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 1907
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (96)...(1211)
/ OTHER INFORMATION: Human epithelial-restricted with serine box (ESX)
/ OTHER INFORMATION: protein.
US-09-570-593-4

Alignment Scores:
Pred. No.: 2.1e-05 Length: 1907
Score: 84.00 Matches: 16
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Matches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-08-978-217-12 (1-16) x US-09-570-593-4 (1-1907)

QY 1 LysAsnSerSerGlyTrypYsgIugIuValLeuGlnSerArgAsn 16
DB 1161 AAAAAGCTCAAGCGGCTGGAAGAGAGAGAGGTTCTCCAGATCGGAC 1208

RESULT 5
US-08-746-789A-1

Sequence 1, Application US/08746789A

Patent No. 5789200

GENERAL INFORMATION:

APPLICANT: Iemai Kola, Martin J. Tyms, Christine Debouck

TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELP3

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road, P.O. Box 1539

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

SOFTWARE: MICROSOFT WORD

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/746,789A

FILING DATE: No. 5789200ember 15, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: William T. Han

REGISTRATION NUMBER: 34,344

REFERENCE/DOCKET NUMBER: ATG 50024

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610 270 5219

TELEFAX: 610 270 4026

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1920

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: NO

US-08-746-789A-1

Alignment Scores:

Pred. No.: 2,12e-05 Length: 1920

Score: 84.00 Matches: 16

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-08-978-217-12 (1-16) x US-08-746-789A-1 (1-1920)

QY 1 LysAsnSerSerGlyTrypYsgIugIuValLeuGlnSerArgAsn 16

DB 1180 AAAAAGCTCAAGCGGCTGGAAGAGAGAGGTTCTCCAGATCGGAC 1227

APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240,409

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL Program

SEQ ID NO 959

LENGTH: 2719

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6673549 337058.1

LOCATION: 479

OTHER INFORMATION: a, t, c, g, or other

US-09-976-594-959

Alignment Scores:

Pred. No.: 101 Length: 2719

Score: 47.00 Matches: 9

Percent Similarity: 62.50% Conservative: 1

Best Local Similarity: 56.25% Mismatches: 6

Query Match: 55.95% Indels: 0

DB: 4 Gaps: 0

US-08-978-217-12 (1-16) x US-09-976-594-959 (1-2719)

QY 1 LysAsnSerSerGlyTrypYsgIugIuValLeuGlnSerArgAsn 16

DB 1073 AAAAATGGGGGGGGGTGGAAGAGCTGATGTAATGCTTATAT 120

RESULT 7
US-09-822-871-3

Sequence 3, Application US/09822871

Patent No. 6723547

GENERAL INFORMATION:

APPLICANT: WEBSTER, Marion et al

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,

FILE REFERENCE: CL001219

CURRENT APPLICATION NUMBER: US/09/822,871

CURRENT FILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 254366

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(254366)

OTHER INFORMATION: n = A,T,C or G

US-09-822-871-3

Alignment Scores:

Pred. No.: 2,21e+04 Length: 254366

Score: 47.00 Matches: 9

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 90.00% Mismatches: 0

Query Match: 55.95% Indels: 0

DB: 4 Gaps: 0

US-08-978-217-12 (1-16) x US-09-822-871-3 (1-254366)

QY 7 LysGluGluGluValLeuGlnSerArgAsn 16

DB 200592 AAAAGAGGAGATTTTCAAAAGCAGGAC 200621

RESULT 8
US-09-638-649-6/c
; Sequence 6, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (PAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: US/09/638,649
; FILE REFERENCE: 05/75/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1348
; TYPE: DNA
; ORGANISM: Murine
US-09-638-649-6

Alignment Scores:
Pred. No.: 66 Length: 1348
Score: 46.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.76% Indels: 0
Gaps: 0
DB: 4

US-08-978-217-12 (1-16) x US-09-638-649-6 (1-1348)

Qy 2 AaSeSerGlyTrpLyseGluGlu 9
Db 275 AATTCAGTGGCTGAGAGGAG 252

RESULT 9
US-09-554-337-4
; Sequence 4, Application US/09554337
; Patent No. 6475780
; GENERAL INFORMATION:
; APPLICANT: Partridge, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michael H.
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: 1038-1042 MIS
; CURRENT APPLICATION NUMBER: US/09/554,337
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/065,791
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: PCT/CA98/01064
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: respiratory syncytial virus
US-09-554-337-4

Alignment Scores:
Pred. No.: 555 Length: 8100
Score: 46.00 Matches: 7
Percent Similarity: 85.71% Conservative: 5
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 54.76% Indels: 0
Gaps: 0

US-08-978-217-12 (1-16) x US-09-554-337-4 (1-8100)

Qy 3 SeSerGlyTrpLyseGluGluValLeuGlnSerArgAsn 16
Db 3 SeSerGlyTrpLyseGluGluValLeuGlnSerArgAsn 16

Db 397 GCCACAACTGGGCGGAGGAGGAGGTTTACAGCCGAGGAGAC 438

RESULT 10
US-07-920-281C-1
; Sequence 1, Application US/07920281C
; Patent No. 5739026
; GENERAL INFORMATION:
; APPLICANT: Garoff, Henrik
; APPLICANT: Liljestrom, Peter
; TITLE OF INVENTION: DNA Expression Systems Based on
; TITLE OF INVENTION: Alphaviruses
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,281C
; FILING DATE: 13-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 828-103P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TUBE: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Semliki Forest Virus
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..11517
; OTHER INFORMATION: /label= genome
; OTHER INFORMATION: /note= "Semliki Forest Virus complete nucleotide
; OTHER INFORMATION: sequence, presented as a cloned DNA sequence; see
; OTHER INFORMATION: Figure 5."
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 87..7379
; OTHER INFORMATION: /product= "SFV polyprotein"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7421..11179
; OTHER INFORMATION: /product= "SFV polyprotein"
US-07-920-281C-1

Alignment Scores:
Pred. No.: 843 Length: 11517
Score: 46.00 Matches: 7
Percent Similarity: 85.71% Conservative: 5
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 54.76% Indels: 0
Gaps: 0

US-08-978-217-12 (1-16) x US-07-920-281C-1 (1-11517)


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; LOCATION: 7421..11179
; OTHER INFORMATION: /product= "SFV polyprotein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-688-842-1

Alignment Scores:
Pred. No.: 843 Length: 11517
Score: 46.00 Matches: 7
Percent Similarity: 85.71% Conservative: 5
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 54.76% Indels: 0
DB: 4 Gaps: 0

US-08-978-217-12 (1-16) x US-09-688-842-1 (1-11517)

QY 3 SerSerGlyTTrpLysGluGluValLeuGlnSerArgAsn 16
Db 675 GCCCAAACTGGGCCGACGACGAGTGTTCACAGCCAGAAC 716

RESULT 13
US-09-554-337-1
; Sequence 1, Application US/09554337
; Patent No. 6475780
; GENERAL INFORMATION:
; APPLICANT: Partridge, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel H.
; FILE REFERENCE: 1038-1042 MIS
; CURRENT APPLICATION NUMBER: US/09/554,337
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/065,791
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: PCT/CA98/01064
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15538
; TYPE: DNA
; ORGANISM: respiratory syncytial virus
US-09-554-337-1

Alignment Scores:
Pred. No.: 1,2e+03 Length: 15538
Score: 46.00 Matches: 7
Percent Similarity: 85.71% Conservative: 5
Best Local Similarity: 50.00% Mismatches: 2
Query Match: 54.76% Indels: 0
DB: 4 Gaps: 0

US-08-978-217-12 (1-16) x US-09-554-337-1 (1-15538)

QY 3 SerSerGlyTTrpLysGluGluValLeuGlnSerArgAsn 16
Db 3221 GCCCAAACTGGGCCGACGACGAGTGTTCACAGCCAGAAC 3262

RESULT 14
US-09-464-535-25/C
; Sequence 25, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalecki, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: B81306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
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; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Glycine max
US-09-464-535-25

Alignment Scores:
Pred. No.: 68.7 Length: 993
Score: 45.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 53.57% Indels: 0
DB: 4 Gaps: 0

US-08-978-217-12 (1-16) x US-09-464-535-25 (1-993)

QY 2 AsnSerSerGlyTTrpLysGluGluValLeuGlnSerArg 15
Db 661 TCCAGCAGCGGATGGCAATGATCAAGGATATTACATCCAGG 620

RESULT 15
US-09-299-141-5/C
; Sequence 5, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, STRONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; PRIOR FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
US-09-299-141-5

Alignment Scores:
Pred. No.: 758 Length: 7492
Score: 45.00 Matches: 10
Percent Similarity: 61.90% Conservative: 3
Best Local Similarity: 47.62% Mismatches: 2
Query Match: 53.57% Indels: 6
DB: 4 Gaps: 1

US-08-978-217-12 (1-16) x US-09-299-141-5 (1-7492)

QY 2 AsnSerSerGlyTTrp-----LysGluGluGluValLeuGlnSerArg 15
Db 813 AACAGCTCAGGCTGTTGATGCAACTTACCTTTAAAGAAATGTAATTCACCAAGCAAA 754

QY 16 Asn 16
Db 753 AAC 751

Search completed: November 15, 2004, 23:13:46
Job time : 27.9406 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 21:57:02 ; Search time 141.363 Seconds
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3209.338 Million cell updates/sec

Title: US-08-978-217-7

Perfect score: 445
Sequence: 1 NCLEBRLVFGPLGQDLA.....ELUDGQASPHYRPGSCAG 84

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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3625171 segs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	445	100.0	563	9	US-09-922-217-944
C 2	445	100.0	563	9	US-09-833-263-944
C 3	445	100.0	563	13	US-10-025-360-944
C 4	445	100.0	626	9	US-09-922-217-853
C 5	445	100.0	626	9	US-09-833-263-853
C 6	445	100.0	626	13	US-10-025-380-853
C 7	445	100.0	1307	14	US-10-097-380-74
C 8	445	100.0	1307	15	US-10-291-808-27
C 9	445	100.0	1915	9	US-09-964-824A-101
C 10	445	100.0	1915	9	US-09-964-824A-563
C 11	445	100.0	1915	9	US-09-880-107-3420
C 12	445	100.0	1915	9	US-09-967-768A-192
C 13	445	100.0	1917	3	US-09-922-217-1105
C 14	445	100.0	1917	13	US-10-025-380-1105
C 15	445	100.0	1956	16	US-10-264-049-756
C 16	445	100.0	1956	9	US-09-925-301-207
C 17	445	100.0	2269	15	US-10-131-410-64
C 18	439	98.7	355	9	US-09-867-701-4818
C 19	305	68.5	174	9	US-09-998-598-1740
C 20	111	24.9	437	9	US-09-998-598-2216
C 21	84	18.9	641	13	US-10-027-632-199194
C 22	84	18.9	641	13	US-10-027-632-199195
C 23	84	18.9	641	13	US-10-027-632-199196
C 24	84	18.9	641	13	US-10-027-632-199197
C 25	84	18.9	641	13	US-10-027-632-199198
C 26	84	18.9	641	15	US-10-027-632-199194
C 27	84	18.9	641	15	US-10-027-632-199195
C 28	84	18.9	641	15	US-10-027-632-199196
C 29	84	18.9	641	15	US-10-027-632-199197
C 30	84	18.9	641	15	US-10-027-632-199198
C 31	73.5	16.5	624	16	US-10-282-122A-7521
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C 33	73.5	16.5	902568	15	US-10-156-761-1
C 34	73	16.4	1005	15	US-10-369-493-40562
C 35	73	16.4	2746	17	US-10-433-171-7
C 36	72.5	16.3	1637	17	US-10-437-963-92512
C 37	72.5	16.3	2770	16	US-10-287-226-329
C 38	72.5	16.3	51705	16	US-10-052-482-229
C 39	72.5	16.3	353	9	US-09-854-133-195
C 40	72	16.2	398	9	US-09-854-133-697
C 41	72	16.2	398	15	US-10-144-649A-697
C 42	72	16.2	407	10	US-09-918-995-36824
C 43	72	16.2	410	10	US-09-918-995-16413
C 44	72	16.2	521	9	US-09-884-441-139
C 45	72	16.2	521	9	US-09-884-441-139

ALIGNMENTS

RESULT 1
US-09-922-217-944/c
Sequence 944, Application US/09922217
Patient No. US2002007641A41
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeline Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Yiang, Yugu
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922, 217

;; CURRENT FILING DATE: 2001-08-03
;; NUMBER OF SEQ ID NOS: 1124
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 944
;; LENGTH: 563
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-922-217-944

Alignment Scores:

Pred. No.:	1,72e-55	Length:	563
Score:	445.00	Matches:	84
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-08-978-217-7 (1-84) x US-09-922-217-944 (1-563)

QY 1 AenCyAAlaLeuGluGluLeuAArgLeuValPheGlyProLeuGlyAAspGlnLeuHsAla 20
Db 472 AATTGTGCCCTTGAGAGAGCTGCGTCTGTGGGCTCTGGGGGAGCAACTCCATGCC 413
QY 21 GlnLeuAArgAspLeuThrSerSerSerSerAAspGluLeuSerTrpIleIleGluLeu 40
Db 412 CAGCTCGAGAGACCTCACTTCCAGCTCTTGATGAGCTCAGTTGATCATTGAGCTGCTG 353
QY 41 GlnLeuAAspGlyMetAlaPheGlnGlnAlaLeuAAspProGlyProPheAAspGlnGlySer 60
Db 352 GAGAAAGATGAGATGAGCTGCTTCCAGAGAGCCCTTAACCAAGAGCCCTTGAACAGAGGAGC 233
QY 61 ProPheAAlaGlnGluLeuLeuAAspAAspGlyGlnGlnAlaLeuAAspProGlyProGlySer 80
Db 292 CCTTGTCCAGAGAGCTGCTGAGAGAGCTGAGAGAGCCCTTCAACCCCGGAGC 233
QY 81 CyegIyAlaGly 84
Db 232 TGTGGCCGAGGA 221

RESULT 2

US-09-833-263-944/C
; Sequence 944, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeline J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 944
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-263-944

Alignment Scores:

Pred. No.:	1,72e-55	Length:	563
Score:	445.00	Matches:	84
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-08-978-217-7 (1-84) x US-09-833-263-944 (1-563)

QY 1 AenCyAAlaLeuGluGluLeuAArgLeuValPheGlyProLeuGlyAAspGlnLeuHsAla 20
Db 472 AATTGTGCCCTTGAGAGAGCTGCGTCTGTGGGCTCTGGGGGAGCAACTCCATGCC 413
QY 21 GlnLeuAArgAspLeuThrSerSerSerSerAAspGluLeuSerTrpIleIleGluLeu 40
Db 412 CAGCTCGAGAGACCTCACTTCCAGCTCTTGATGAGCTCAGTTGATCATTGAGCTGCTG 353
QY 41 GlnLeuAAspGlyMetAlaPheGlnGlnAlaLeuAAspProGlyProPheAAspGlnGlySer 60
Db 352 GAGAAAGATGAGATGAGCTGCTTCCAGAGAGCCCTTAACCAAGAGCCCTTGAACAGAGGAGC 233
QY 61 ProPheAAlaGlnGluLeuLeuAAspAAspGlyGlnGlnAlaLeuAAspProGlyProGlySer 80
Db 292 CCTTGTCCAGAGAGCTGCTGAGAGAGCTGAGAGAGCCCTTCAACCCCGGAGC 233
QY 81 CyegIyAlaGly 84
Db 232 TGTGGCCGAGGA 221

RESULT 3

US-10-025-380-944/C
; Sequence 944, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skelky, Yaelir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 944
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-944

Alignment Scores:

Pred. No.:	1,72e-55	Length:	563
Score:	445.00	Matches:	84
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-08-978-217-7 (1-84) x US-10-025-380-944 (1-563)

QY 1 AenCyAAlaLeuGluGluLeuAArgLeuValPheGlyProLeuGlyAAspGlnLeuHsAla 20
Db 472 AATTGTGCCCTTGAGAGAGCTGCGTCTGTGGGCTCTGGGGGAGCAACTCCATGCC 413
QY 21 GlnLeuAArgAspLeuThrSerSerSerSerAAspGluLeuSerTrpIleIleGluLeu 40
Db 412 CAGCTCGAGAGACCTCACTTCCAGCTCTTGATGAGCTCAGTTGATCATTGAGCTGCTG 353
QY 41 GlnLeuAAspGlyMetAlaPheGlnGlnAlaLeuAAspProGlyProPheAAspGlnGlySer 60
Db 352 GAGAAAGATGAGATGAGCTGCTTCCAGAGAGCCCTTAACCAAGAGCCCTTGAACAGAGGAGC 233

QY 61 ProPha1aGlnGluLeuLeuAaPspGlyGlnGlnAlaSerProTyrHisProGlySer 80
Db 292 CCCTTGCCCGAGAGCTGCTGAGACGACGCTCAGACCAACCCCTTACCAACCCCGGACG 233
QY 81 CygGlyAlaGly 84
Db 232 TGTGGCGCAGGA 221

RESULT 4

US-09-922-217-853/C
; Sequence 853, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yudi
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 853
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-853

Alignment Scores:
Pred. No.: 1,97e-55 Length: 626
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-978-217-7 (1-84) x US-09-922-217-853 (1-626)

QY 1 AaTCyAlaLeuGlnGluLeuAaPspGlyGlnGlnAlaSerProTyrHisProGlySer 20
Db 471 AATTGTGCTTGAAGAGCTGCTGCTGCTTGTGGGGCTTGGGGGACCACTCCATGCC 412
QY 21 GlnLeuAaPspGlyMetAlaPheGlnGlnAlaLeuAaPspGlyProGlySer 40
Db 411 CAGCTGGAGACCTCCTCAGCTCTTCTGATGAGCTCAGCTTGATCATTGAGCTGCTG 352
QY 41 GlnLeuAaPspGlyMetAlaPheGlnGlnAlaLeuAaPspGlyProGlySer 60
Db 351 GAGAGAGATGCGATGGCTTCCAGAGAGCCCTTACAGAGGCGCTTGAACAGGGCAGC 292
QY 61 ProPha1aGlnGlnGluLeuLeuAaPspGlyGlnGlnAlaSerProTyrHisProGlySer 80
Db 291 CCCTTGCCCGAGAGCTGCTGAGACGACGCTCAGCAAGCCAGCCCTTACCAACCCCGGACG 232
QY 81 CygGlyAlaGly 84
Db 231 TGTGGCGCAGGA 220

RESULT 5
US-09-833-263-853/C
; Sequence 853, Application US/09833263
; Patent No. US20020110547A1

; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeline J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-853

Alignment Scores:
Pred. No.: 1,97e-55 Length: 626
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-978-217-7 (1-84) x US-09-833-263-853 (1-626)

QY 1 AaTCyAlaLeuGlnGluLeuAaPspGlyGlnGlnAlaSerProGlyAaPspGlnLeuHisAla 20
Db 471 AATTGTGCTTGAAGAGCTGCTGCTGCTTGTGGGGCTTGGGGGACCACTCCATGCC 412
QY 21 GlnLeuAaPspGlyMetAlaPheGlnGlnAlaLeuAaPspGlyProGlySer 40
Db 411 CAGCTGGAGACCTCCTCAGCTCTTCTGATGAGCTCAGCTTGATCATTGAGCTGCTG 352
QY 41 GlnLeuAaPspGlyMetAlaPheGlnGlnAlaLeuAaPspGlyProGlySer 60
Db 351 GAGAGAGATGCGATGGCTTCCAGAGAGCCCTTACAGAGGCGCTTGAACAGGGCAGC 292
QY 61 ProPha1aGlnGlnGluLeuLeuAaPspGlyGlnGlnAlaSerProTyrHisProGlySer 80
Db 291 CCCTTGCCCGAGAGCTGCTGAGACGACGCTCAGCAAGCCAGCCCTTACCAACCCCGGACG 232
QY 81 CygGlyAlaGly 84
Db 231 TGTGGCGCAGGA 220

RESULT 6

US-10-025-380-853/C
; Sequence 853, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yudi
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yaser A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380

Alignment Scores:
Pred. No.: 8.11e-55 Length: 1907
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-08-978-217-7 (1-84) x US-10-291-808-27 (1-1907)

QY 1 AsnCysAlaLeuGluGluLeuAlaGluValPheGlyProLeuGlyAspGlnLeuHisAla 20
DB 405 AATTGGCCCTTGAAGAGAGCTGCTGCTTGGGCTCTTGGGGAGCAACCTCCATGCC 464
QY 21 GlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIleGluLeu 40
DB 465 CAGCTCGAGACTCCTCCTCCAGCTCTTGTGATGAGCTCACTTGATCATTGAGCTGCTG 524
QY 41 GluLyAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySer 60
DB 525 GAGAAGATGGAGCTGCTGCTCCAGAGGCTTGAAGCCAGGCTTGAAGAGGAGCAGC 584
QY 61 ProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySer 80
DB 585 CCTTTGCCAGAGCTGCTGAGACGAGTCAAGCAAGCCCTTACCAACCCCGGAGC 644
QY 81 CysGlyAlaGly 84
DB 645 TGTGGCGCAGGA 656

RESULT 9

US-09-964-824A-101
Sequence 101, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:

APPLICANT: Horriagan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964, 824A
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236, 033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236, 032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236, 028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: Patentin version 3.0
SEQ ID NO 101
LENGTH: 1915
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-824A-101

Alignment Scores:
Pred. No.: 8.16e-55 Length: 1915
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-978-217-7 (1-84) x US-09-964-824A-101 (1-1915)

QY 1 AsnCysAlaLeuGluGluLeuAlaGluValPheGlyProLeuGlyAspGlnLeuHisAla 20
DB 429 AATTGGCCCTTGAAGAGAGCTGCTGCTTGGGCTCTTGGGGAGCAACCTCCATGCC 488
QY 21 GlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIleGluLeu 40
DB 489 CAGCTCGAGACTCCTCCTCCAGCTCTTGTGATGAGCTCACTTGATCATTGAGCTGCTG 548

QY 41 GluLyAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySer 60
DB 549 GAGAAGATGGAGCTGCTTCCAGAGGCTTGAAGCCAGGCTTGAAGAGGAGCAGC 608
QY 61 ProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySer 80
DB 609 CCTTTGCCAGAGCTGCTGAGACGAGTCAAGCAAGCCCTTACCAACCCCGGAGC 668

QY 81 CysGlyAlaGly 84
DB 669 TGTGGCGCAGGA 680

RESULT 10

US-09-964-824A-563
Sequence 563, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:

APPLICANT: Horriagan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964, 824A
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236, 033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236, 032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236, 028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: Patentin version 3.0
SEQ ID NO 563
LENGTH: 1915
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-824A-563

Alignment Scores:
Pred. No.: 8.16e-55 Length: 1915
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-978-217-7 (1-84) x US-09-964-824A-563 (1-1915)

QY 1 AsnCysAlaLeuGluGluLeuAlaGluValPheGlyProLeuGlyAspGlnLeuHisAla 20
DB 429 AATTGGCCCTTGAAGAGAGCTGCTGCTTGGGCTCTTGGGGAGCAACCTCCATGCC 488
QY 21 GlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIleGluLeu 40
DB 489 CAGCTCGAGACTCCTCCTCCAGCTCTTGTGATGAGCTCACTTGATCATTGAGCTGCTG 548
QY 41 GluLyAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySer 60
DB 549 GAGAAGATGGAGCTGCTTCCAGAGGCTTGAAGCCAGGCTTGAAGAGGAGCAGC 608
QY 61 ProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySer 80
DB 609 CCTTTGCCAGAGCTGCTGAGACGAGTCAAGCAAGCCCTTACCAACCCCGGAGC 668
QY 81 CysGlyAlaGly 84
DB 669 TGTGGCGCAGGA 680

RESULT 11

US-09-880-107-3420
Sequence 3420, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.

```

; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3420
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843
US-09-880-107-3420
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Alignment Scores:
Pred. No.: 8,16e-55 Length: 1915
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-08-978-217-7 (1-84) x US-09-880-107-3420 (1-1915)

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QY 1 AsnCysAlaLeuGluGluLeuAArgLeuValPheGlyProLeuGlyAspGlnLeuHisAla 20
Db 429 AATTGGCCCTTAGAGAGCTGCGCTGTGCTTTGGGCTCTGGGGAGCAACTCCATGCC 488
QY 21 GlnLeuAArgAspLeuThrSerSerSerSerSerAspGlnLeuSerTrpIleIleGlnLeu 40
Db 489 CAGCTCGAGACCTCACTTCAGCTCTTGATGAGCTCAGTTGATGATGAGCTGCTG 548
QY 41 GlnLeuAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySer 60
Db 549 GAGAGAGATGGATGGCTTCCAGAGAGCCCTTAGACCAAGCCCTTTGACCAAGGAGC 608
QY 61 ProPheAlaGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerProGlyHisProGlySer 80
Db 609 CCCTTGGCCAGAGAGCTGCTGAGAGAGCTGAGCAAGCAAGCCCTTACCAAGCCGAGC 668
QY 81 CysGlyAlaGly 84
Db 669 TGTGGCGCAGGA 680
```

RESULT 12

```

US-09-967-768A-192
; Sequence 192, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 192
; LENGTH: 1915
; TYPE: DNA
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```

; ORGANISM: Homo sapiens
US-09-967-768A-192
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```

Alignment Scores:
Pred. No.: 8,16e-55 Length: 1915
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-08-978-217-7 (1-84) x US-09-967-768A-192 (1-1915)

```

QY 1 AsnCysAlaLeuGluGluLeuAArgLeuValPheGlyProLeuGlyAspGlnLeuHisAla 20
Db 429 AATTGGCCCTTAGAGAGCTGCGCTGTGCTTTGGGCTCTGGGGAGCAACTCCATGCC 488
QY 21 GlnLeuAArgAspLeuThrSerSerSerSerSerAspGlnLeuSerTrpIleIleGlnLeu 40
Db 489 CAGCTCGAGACCTCACTTCAGCTCTTGATGAGCTCAGTTGATGATGAGCTGCTG 548
QY 41 GlnLeuAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySer 60
Db 549 GAGAGAGATGGATGGCTTCCAGAGAGCCCTTAGACCAAGCCCTTTGACCAAGGAGC 608
QY 61 ProPheAlaGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerProGlyHisProGlySer 80
Db 609 CCCTTGGCCAGAGAGCTGCTGAGAGAGCTGAGCAAGCAAGCCCTTACCAAGCCGAGC 668
QY 81 CysGlyAlaGly 84
Db 669 TGTGGCGCAGGA 680
```

RESULT 13

```

US-09-922-217-1105
; Sequence 1105, Application US/09922217
; Patent No. US2002076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121,471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-1105
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```

Alignment Scores:
Pred. No.: 8,17e-55 Length: 1917
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-08-978-217-7 (1-84) x US-09-922-217-1105 (1-1917)

Qy 1 AsnCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGlnLeuHisAla 20
Db 431 AATTGTCCTTGAAGAGCTGCGTCTGCTTTGGGCTTGGGGGACCAACTCCATGCC 490
Qy 21 GlnLeuArgAspLeuThrSerSerSerSerAspGlnLeuSerTrpIleIleGluLeu 40
Db 491 CAGCTCGAGACCTCACTTCACGCTCTTGATGAGCTCAGATTCATTGAGCTGCTG 550
Qy 41 GlnLeuAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySer 60
Db 551 GAGAGAGATGAGCTGCGCTTCCAGAGAGCCCTTGAAGCCAGGCTTTTGACAGGGCAGC 610
Qy 61 ProPheAlaGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerProTyrlHisProGlySer 80
Db 611 CCTTTGCCAGAGAGCTGCTGAGACGCTTCAGCAAGCCAGCCCTTACACCCCGGAGC 670
Qy 81 CysGlyAlaGly 84
Db 671 TGTGGCGCAGGA 682
RESULT 14
US-10-025-380-1105
; Sequence 1105, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodee, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Ranger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-1105
Alignment Scores:
Pred. No.: 8.17e-55 Length: 1917
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 13
US-08-978-217-7 (1-84) x US-10-025-380-1105 (1-1917)
Qy 1 AsnCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGlnLeuHisAla 20
Db 431 AATTGTCCTTGAAGAGCTGCGTCTGCTTTGGGCTTGGGGGACCAACTCCATGCC 490
Qy 21 GlnLeuArgAspLeuThrSerSerSerSerAspGlnLeuSerTrpIleIleGluLeu 40
Db 491 CAGCTCGAGACCTCACTTCACGCTCTTGATGAGCTCAGATTCATTGAGCTGCTG 550
Qy 41 GlnLeuAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySer 60
Db 551 GAGAGAGATGAGCTGCGCTTCCAGAGAGCCCTTGAAGCCAGGCTTTTGACAGGGCAGC 610

Db 551 GAGAGAGATGAGCTGCGCTTCCAGAGAGCCCTTGAAGCCAGGCTTTTACAGGCGCAGC 610
Qy 61 ProPheAlaGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerProTyrlHisProGlySer 80
Db 611 CCTTTGCCAGAGAGCTGCTGAGACGCTTCAGCAAGCCAGCCCTTACACCCCGGAGC 670
Qy 81 CysGlyAlaGly 84
Db 671 TGTGGCGCAGGA 682
RESULT 15
US-10-264-049-756
; Sequence 756, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264.049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 756
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-049-756
Alignment Scores:
Pred. No.: 8.38e-55 Length: 1956
Score: 445.00 Matches: 84
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 16
US-08-978-217-7 (1-84) x US-10-264-049-756 (1-1956)
Qy 1 AsnCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGlnLeuHisAla 20
Db 470 AATTGTCCTTGAAGAGCTGCGTCTGCTTTGGGCTTGGGGGACCAACTCCATGCC 529
Qy 21 GlnLeuArgAspLeuThrSerSerSerSerAspGlnLeuSerTrpIleIleGluLeu 40
Db 530 CAGCTCGAGACCTCACTTCACGCTCTTGATGAGCTCAGTTCATTGAGCTGCTG 589
Qy 41 GlnLeuAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySer 60
Db 590 GAGAGAGATGAGCTGCGCTTCCAGAGAGCCCTTGAAGCCAGGCTTTTGACAGGGCAGC 649
Qy 61 ProPheAlaGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerProTyrlHisProGlySer 80
Db 650 CCTTTGCCAGAGAGCTGCTGAGACGCTTCAGCAAGCCAGCCCTTACACCCCGGAGC 709
Qy 81 CysGlyAlaGly 84
Db 710 TGTGGCGCAGGA 721
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Title: US-08-978-217-7

Perfect score: 445
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_NA -QFMT=faastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bloms62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALLCN=15
-MODE=LOCAL -OUTFILE=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08978217@cgn_1.1_213@runat_15112004_103131_12764 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445	100.0	1907	4	US-09-300-958A-27
2	445	100.0	1907	4	US-09-570-593-4
3	445	100.0	1920	1	US-08-746-789A-1
4	76.5	17.2	631	4	US-09-513-999C-10263
5	73.5	16.5	624	4	US-09-252-991A-13629
6	73.5	16.5	801	4	US-09-252-991A-13619
7	72	16.2	398	4	US-09-854-133-697
8	72	16.2	521	4	US-09-404-879A-139
9	72	16.2	521	4	US-09-338-933-139
10	72	16.2	521	4	US-09-215-681-139
11	72	16.2	521	4	US-09-216-003A-139
12	72	16.2	521	4	US-09-667-857-139

C 13	72	16.2	551	4	US-09-404-879A-92	Sequence 92, App1
C 14	72	16.2	551	4	US-09-338-933-92	Sequence 92, App1
C 15	72	16.2	551	4	US-09-215-681-92	Sequence 92, App1
C 16	72	16.2	551	4	US-09-216-003A-92	Sequence 92, App1
C 17	72	16.2	551	4	US-09-667-857-92	Sequence 92, App1
C 18	72	16.2	555	4	US-09-404-879A-107	Sequence 107, App
C 19	72	16.2	555	4	US-09-338-933-107	Sequence 107, App
C 20	72	16.2	555	4	US-09-215-681-107	Sequence 107, App
C 21	72	16.2	555	4	US-09-216-003A-107	Sequence 107, App
C 22	72	16.2	555	4	US-09-667-857-107	Sequence 107, App
C 23	72	16.2	2301	1	US-08-306-691B-23	Sequence 23, App1
C 24	72	16.2	2301	4	US-09-167-206-3	Sequence 3, App1
C 25	72	16.2	2301	5	PCT-US93-06251-78	Sequence 78, App1
C 26	71.5	16.1	3141	2	US-08-956-242-1	Sequence 1, App1
C 27	71.5	16.1	3141	3	US-09-351-215-1	Sequence 1, App1
C 28	70.5	15.8	4819	4	US-09-774-528-72	Sequence 72, App1
C 29	69.5	15.6	1412	4	US-09-799-451-426	Sequence 426, App
C 30	67.5	15.2	1011	4	US-09-252-991A-7550	Sequence 7550, Ap
C 31	67.5	15.2	1062	4	US-09-252-991A-7788	Sequence 7788, Ap
C 32	66.5	14.9	534	4	US-09-252-991A-12113	Sequence 12113, A
C 33	66.5	14.9	624	4	US-09-252-991A-12252	Sequence 12252, A
C 34	66.5	14.9	849	4	US-09-252-991A-11100	Sequence 11100, A
C 35	66.5	14.9	852	4	US-09-252-991A-10964	Sequence 10964, A
C 36	66.5	14.9	1473	4	US-09-518-914-7	Sequence 7, App1
C 37	66	14.8	1594	2	US-08-955-713-1	Sequence 1, App1
C 38	66	14.8	4154	1	US-08-131-365B-37	Sequence 37, App1
C 39	66	14.8	4154	2	US-08-668-123-37	Sequence 37, App1
C 40	66	14.8	6732	4	US-09-976-594-99	Sequence 99, App1
C 41	66	14.8	114793	4	US-10-148-806-3	Sequence 3, App1
C 42	65.5	14.7	444	4	US-09-252-991A-7864	Sequence 7864, Ap
C 43	65.5	14.7	1185	4	US-09-270-767-12737	Sequence 12737, A
C 44	65.5	14.7	11282	3	US-09-754-250-3	Sequence 3, App1
C 45	65	14.6	661	4	US-10-101-464A-202	Sequence 202, App

ALIGNMENTS

RESULT 1
US-09-300-958A-27
; Sequence 27, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: Mclelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-27
Alignment Scores:
Pred. No.: 1,56e-53
Score: 445.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 1907
Matches: 84
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
US-08-978-217-7 (1-84) x US-09-300-958A-27 (1-1907)

QY 1 AencCyAlaLeuGluGluLeuValPheGlyProLeuGlyAaspGlnLeuHsAla 20
DB 405 AATTGTGCGCTTGAGAGAGCTGCGCTGTCTTTGGGCTCTGGGGAGCAACTCCAGTCC 464
QY 21 GlnLeuArgAspLeuThrSerSerSerSerAaspGlnLeuSerTrpIleIleGlnLeuLeu 40
DB 465 CAGCTGCGAGACCTTCAGCTCTTGTGATGAGCTCAGTTGGATCATTTAGCTGCTG 524
QY 41 GlnLeuArgAspLeuThrSerSerSerSerAaspGlnLeuSerProGlyProPheAspGlnGlySer 60
DB 525 GAGAGAGATGAGAGAGCTGCTTCAGAGAGCCCTAGACCCAGGAGCCCTTTGACCAAGGAGC 584
QY 61 ProPheAlaGlnGluLeuLeuAaspAaspGlyGlnGlnAlaSerProGlyTrpHisProGlySer 80
DB 585 CCGTTTCCAGAGAGCTGCTGAGAGAGCTGAGAGAGCCCTTACCAAGCCCGGAGC 644
QY 81 CyeglyAlaGly 84
DB 645 TGTGGCCGAGGA 656

RESULT 2

US-09-570-593-4
; Sequence 4, Application US/09570593
; Patent No. 6566063
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Hartowe, Greg
; TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
; FILE REFERENCE: 2300-1556
; CURRENT APPLICATION NUMBER: US/09/570, 593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134, 112
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1211)
; OTHER INFORMATION: Human epithelial-restricted with serine box (ESX)
; OTHER INFORMATION: protein.
US-09-570-593-4

Alignment Scores:

Pred. No.:	1.58e-53	Length:	1907
Score:	445.00	Matches:	84
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-08-978-217-7 (1-84) x US-09-570-593-4 (1-1907)

QY 1 AencCyAlaLeuGluGluLeuValPheGlyProLeuGlyAaspGlnLeuHsAla 20
DB 405 AATTGTGCGCTTGAGAGAGCTGCGCTGTCTTTGGGCTCTGGGGAGCAACTCCAGTCC 464
QY 21 GlnLeuArgAspLeuThrSerSerSerSerAaspGlnLeuSerTrpIleIleGlnLeuLeu 40
DB 465 CAGCTGCGAGACCTTCAGCTCTTGTGATGAGCTCAGTTGGATCATTTAGCTGCTG 524
QY 41 GlnLeuArgAspLeuThrSerSerSerSerAaspGlnLeuSerProGlyProPheAspGlnGlySer 60
DB 525 GAGAGAGATGAGAGAGCTGCTTCAGAGAGCCCTAGACCCAGGAGCCCTTTGACCAAGGAGC 584
QY 61 ProPheAlaGlnGluLeuLeuAaspAaspGlyGlnGlnAlaSerProGlyTrpHisProGlySer 80

DB 585 CCGTTTCCAGAGAGCTGCTGAGAGAGCTGAGAGAGCCCTTACCAAGCCCGGAGC 644
QY 81 CyeglyAlaGly 84
DB 645 TGTGGCCGAGGA 656

RESULT 3

US-08-746-789A-1
; Sequence 1, Application US/08746789A
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismail Kola, Martin J. Tyms, Christine Debouck
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELF3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746, 789A
; FILING DATE: No. 5789200ember 15, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG 50024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5219
; TELEFAX: 610 270 4026
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; ANTI-SENSE: NO
US-08-746-789A-1

Alignment Scores:

Pred. No.:	1.58e-53	Length:	1920
Score:	445.00	Matches:	84
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-08-978-217-7 (1-84) x US-08-746-789A-1 (1-1920)

QY 1 AencCyAlaLeuGluGluLeuValPheGlyProLeuGlyAaspGlnLeuHsAla 20
DB 424 AATTGTGCGCTTGAGAGAGCTGCGCTGTCTTTGGGCTCTGGGGAGCAACTCCAGTCC 483
QY 21 GlnLeuArgAspLeuThrSerSerSerSerAaspGlnLeuSerTrpIleIleGlnLeuLeu 40
DB 484 CAGCTGCGAGACCTTCAGCTCTTGTGATGAGCTCAGTTGGATCATTTAGCTGCTG 543
QY 41 GlnLeuArgAspLeuThrSerSerSerSerAaspGlnLeuSerProGlyProPheAspGlnGlySer 60
DB 544 GAGAGAGATGAGAGAGCTGCTTCAGAGAGCCCTAGACCCAGGAGCCCTTTGACCAAGGAGC 603
QY 61 ProPheAlaGlnGluLeuLeuAaspAaspGlyGlnGlnAlaSerProGlyTrpHisProGlySer 80

Db 604 CCCTTCCAGAGCTGTGACGAGCTCAGCAAGCCCTTACACCCCGGAGC 663
QY 81 CAGGlyAlaGly 84
Db 664 TGTGGCGCAGGA 675

RESULT 4

US-09-513-999C-10263/C
; Sequence 10263, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10263
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 221
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 228
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 541
; OTHER INFORMATION: k=g or t
US-09-513-999C-10263

Alignment Scores:

Pred. No.:	0.127	Length:	631
Score:	76.50	Matches:	31
Percent Similarity:	39.42%	Conservative:	10
Best Local Similarity:	29.81%	Mismatches:	31
Query Match:	17.19%	Indels:	32
DB:	4	Gaps:	5

US-08-978-217-7 (1-84) x US-09-513-999C-10263 (1-631)

QY 6 GlnLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
Db 600 GAGCTTCATCTTTCTTCATCTTTTAAGCCCGGTTTCAATACCTTACCTCTCTM 541
QY 23 ArgAspLeuThrSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 42
Db 540 ACTCTCATCTGACGAGCTTTTTCAGC-----TTCTTCAGCTTTTTCAGGAGC 496
QY 43 AspGlyMetAla-----Phe 47
Db 495 AGTGGCCAGGCGCTCCCTGAGCAGGCTCCTTCTTCAACAGCTGATTAAGGTTTC 436
QY 48 GlnGlnAlaLeu-AspProGlyProPheAspGlnGlySerProPheAlaGlnGlnLeu 67
Db 435 AAGGAGGCGCACTCAGCTCAGCTGTT--CCCGGCGCGCCTTCTCCCTCAACTTCT 379
QY 67 uAspAspGlyGlnGlnAlaSerProTyrHis-----ProGlySer 80
Db 378 CGGTGAGGCGGCTAGCTGCTCTCTGATCATCTGCTGCTGCTGCAAGAACCTGATC 319
QY 80 rCYGlyAla 83
Db 80 rCYGlyAla 83

Db 318 TTGCGCTTCA 309

RESULT 5

US-09-252-991A-13629/C
; Sequence 13629, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13629
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13629

Alignment Scores:

Pred. No.:	0.335	Length:	624
Score:	73.50	Matches:	26
Percent Similarity:	47.95%	Conservative:	9
Best Local Similarity:	35.62%	Mismatches:	19
Query Match:	16.52%	Indels:	19
DB:	4	Gaps:	4

US-08-978-217-7 (1-84) x US-09-252-991A-13629 (1-624)

QY 12 GlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerSer 31
Db 165 GGAGTACTTGGCGATGATGATCGCTCCCGCGGCTT----- 124
QY 32 GlnLeuSerTrpIleIleGlnLeuGlnGlyuAspGlyMetAlaPheGlnGlnAlaLeu 51
Db 123 CATCTGAGGCGCTTGTG--GTCAGCAGCATGAGCTCTGAGCTCCAGGCGGCTC 67
QY 52 AspProGlyProPheAspGlnGlySerProPheAlaGlnGlnLeuAspAspGlyGln 71
Db 66 GACCCAGGC-----GGCCGAGTGGAGACAGCAAGATGTGCTCATCTCGGCGCA 16
QY 72 GlnAlaSerProTyrHisProGlySerGlyAlaGly 84
Db 15 CAT-----GGTGCAGGT 4

RESULT 6

US-09-252-991A-13819
; Sequence 13819, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13819
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13819

Alignment Scores:

Pred. No.: 0.476 Length: 801
 Score: 73.50 Matches: 26
 Percent Similarity: 47.95% Conservative: 9
 Best Local Similarity: 35.62% Mismatches: 19
 Query Match: 16.52% Indels: 19
 DB: 4 Gaps: 4

US-08-978-217-7 (1-84) x US-09-252-991A-13819 (1-801)

Qy 12 G1yProlenGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerAsp 31
 Db 508 GGAGTACTTCGCCGATCAGTGCATCGCGCGCGCGCTT-----549
 Qy 32 G1uLeuSerTripletLeuGlnLeuGlnAspGlyMetAlaPheGlnGlnAlaLeu 51
 Db 550 CATCTCCAGGCGCTTGG---GTCACAGACAGATGACCTCTCGGCGCTCCAGCGCGCTC 606
 Qy 52 AspProGlyProPheAspGlnGlySerProPheAlaGlnGlnLeuLeuAspAspGlyGln 71
 Db 607 GACCCAGGC-----GGCGGAGTGGAACAGCAAGAAATTGTCGATCTCGGGCAA 657
 Qy 72 GlnAlaSerProTyRHisProGlySerCyGlyAlaGly 84
 Db 658 CAT-----GGTCCAGGT 669

RESULT 7

US-09-854-133-697/C
 ; Sequence 697, Application US/09854133
 ; Patent No. 6759508
 ; GENERAL INFORMATION:
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Mohamach, Radoch
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Serriest, Heather
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.475C10
 ; CURRENT APPLICATION NUMBER: US/09/854.133
 ; CURRENT FILING DATE: 2001-05-11
 ; NUMBER OF SEQ. ID NOS: 735
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 697
 ; LENGTH: 398
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-854-133-697

Alignment Scores:

Pred. No.: 0.291 Length: 398
 Score: 72.00 Matches: 31
 Percent Similarity: 39.81% Conservative: 10
 Best Local Similarity: 30.10% Mismatches: 32
 Query Match: 16.18% Indels: 31
 DB: 4 Gaps: 5

US-08-978-217-7 (1-84) x US-09-854-133-697 (1-398)

Qy 6 G1uLeuArgLeuValPhe-----G1yProlenGlyAspGlnLeuHisAlaGlnLeu 22
 Db 341 GAGTTCATCTTTCTTCATCTTTTAAGCCCGGCTTTCAATACCTTACTTCTCTC 282
 Qy 23 ArgAspLeuThrSerSerSerSerAspGlnLeuSerTripletLeuGlnLeuGlnLys 42
 Db 281 ACTCTCATCGACAGCTTTTTCAGC-----TTCTTCACAGCTTTTTCAGGCG 237
 Qy 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly---54
 Db 236 AGTGGCCAGGCGCTCTGAGACAGGTCCAGCTTTCTTCAACAGCGATGATCTAGCGTT 177
 Qy 55 -----ProPheAspGlnGlySerProPheAlaGlnGlnLeu 67
 Db 176 CAAGAGGCCACCTCAGCTCTGAGCTGTCCCGGCGCGCTTCTCTCTC-CAACTTCTC 118

Qy 68 AspAspGlyGlnGlnAlaSerProTyRHis-----ProGlySer 80
 Db 117 GCTGAGAGGGGCTCAGCTGCTCTCTCTGATCATCTGCTGCTGACAGACTGATCT 58
 Qy 81 CyGlyAla 83
 Db 57 TGGGCTTCA 49

RESULT 8

US-09-404-879A-139/C
 ; Sequence 139, Application US/09404879A
 ; Patent No. 6468546
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Algate, Paul A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.462C2
 ; CURRENT APPLICATION NUMBER: US/09/404.879A
 ; CURRENT FILING DATE: 1999-09-24
 ; NUMBER OF SEQ. ID NOS: 393
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 139
 ; LENGTH: 521
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(521)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-404-879A-139

Alignment Scores:

Pred. No.: 0.425 Length: 521
 Score: 72.00 Matches: 31
 Percent Similarity: 39.81% Conservative: 10
 Best Local Similarity: 30.10% Mismatches: 32
 Query Match: 16.18% Indels: 31
 DB: 4 Gaps: 5

US-08-978-217-7 (1-84) x US-09-404-879A-139 (1-521)

Qy 6 G1uLeuArgLeuValPhe-----G1yProlenGlyAspGlnLeuHisAlaGlnLeu 22
 Db 333 GAGTTCATCTTTCTTCATCTTTTAAGCCCGGCTTTCAATACCTTACTTCTCTC 274
 Qy 23 ArgAspLeuThrSerSerSerSerAspGlnLeuSerTripletLeuGlnLeuGlnLys 42
 Db 273 ACTCTCATCGACAGCTTTTTCAGC-----TTCTTCACAGCTTTTTCAGGCG 229
 Qy 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly---54
 Db 228 AGTGGCCAGGCGCTCTGAGACAGGTCCAGCTTTCTTCAACAGCGATGATCTAGCGTT 169
 Qy 55 -----ProPheAspGlnGlySerProPheAlaGlnGlnLeu 67
 Db 168 CAAGAGGCCACCTCAGCTCAGCTGCTCCCGGCGCGCTTCTCTCTC-CAACTTCTC 110
 Qy 68 AspAspGlyGlnGlnAlaSerProTyRHis-----ProGlySer 80
 Db 109 GCTGAGAGGGGCTCAGCTGCTCTCTCTGATCATCTGCTGCTGACAGACTGATCT 50
 Qy 81 CyGlyAla 83
 Db 49 TGGGCTTCA 41

RESULT 9

US-09-338-933-139/C
 ; Sequence 139, Application US/09338933
 ; Patent No. 648931
 ; GENERAL INFORMATION:


```

; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(521)
; OTHER INFORMATION: n = A,T,C or G
US-09-338-933-139

Alignment Scores:
Pred. No.: 0.425 Length: 521
Score: 72.00 Matches: 31
Percent Similarity: 39.81% Conservative: 10
Best Local Similarity: 30.10% Mismatches: 32
Query Match: 16.18% Indels: 31
DB: 4 Gaps: 5

US-08-978-217-7 (1-84) x US-09-338-933-139 (1-521)
Qy 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
Db 333 GAGTTCATCTTTTCTTCATCTTTTAAAGCCGGTTTCAATAACCTTACCTCTCTC 274
Qy 23 ArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIleGluLeuGluLys 42
Db 273 ACTCTCATCAGACGCTTTTTCAGC-----TTCTTCACGCTTTTGCAGGGC 229
Qy 43 AspGlyMetAla-----PheGlnGluAlaLeuAspProGly--- 54
Db 228 AGTGGCCAGGCGCTCTGAGACGCGTCCAGCTCTTCTTCAACGAGCTGAACTCAGCGTT 169
Qy 55 -----ProPheAspGlnGlySerProPheAlaGlnGluLeu 67
Db 168 CAGGAGGCCACCTCAGCCTCAGCCTTCCCGGGCCGCTTCTCTCCT-CAACTTCTC 110
Qy 68 AspAspGlyGlnGlnAlaSerProTyrHis-----ProGlySer 80
Db 109 GCTGAGGGCGCTCAGCTCGCTCTGCTGATCATCTGCTGCTGCTGCGAGAACTGATCT 50
Qy 81 CygGlyAla 83
Db 49 TGGCGTTCA 41

RESULT 10
US-09-215-681-139/c
; Sequence 139, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (1)...(521)
; OTHER INFORMATION: n = A,T,C or G
US-09-215-681-139

Alignment Scores:
Pred. No.: 0.425 Length: 521
Score: 72.00 Matches: 31
Percent Similarity: 39.81% Conservative: 10
Best Local Similarity: 30.10% Mismatches: 32
Query Match: 16.18% Indels: 31
DB: 4 Gaps: 5

US-08-978-217-7 (1-84) x US-09-215-681-139 (1-521)
Qy 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
Db 333 GAGTTCATCTTTTCTTCATCTTTTAAAGCCGGTTTCAATAACCTTACCTCTCTC 274
Qy 23 ArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIleGluLeuGluLys 42
Db 273 ACTCTCATCAGACGCTTTTTCAGC-----TTCTTCACGCTTTTGCAGGGC 229
Qy 43 AspGlyMetAla-----PheGlnGluAlaLeuAspProGly--- 54
Db 228 AGTGGCCAGGCGCTCTGAGACGCGTCCAGCTCTTCTTCAACGAGCTGATCCTCAGCGTT 169
Qy 55 -----ProPheAspGlnGlySerProPheAlaGlnGluLeu 67
Db 168 CAGGAGGCCACCTCAGCCTCAGCCTTCCCGGGCCGCTTCTCTCCT-CAACTTCTC 110
Qy 68 AspAspGlyGlnGlnAlaSerProTyrHis-----ProGlySer 80
Db 109 GCTGAGGGCGCTCAGCTCGCTCTGCTGATCATCTGCTGCTGCTGCGAGAACTGATCT 50
Qy 81 CygGlyAla 83
Db 49 TGGCGTTCA 41

RESULT 11
US-09-216-003A-139/c
; Sequence 139, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216,003A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (517)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-216-003A-139

Alignment Scores:
Pred. No.: 0.425 Length: 521
Score: 72.00 Matches: 31
Percent Similarity: 39.81% Conservative: 10
Best Local Similarity: 30.10% Mismatches: 32
Query Match: 16.18% Indels: 31
DB: 4 Gaps: 5

US-08-978-217-7 (1-84) x US-09-216-003A-139 (1-521)
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QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
DB 333 GAGTTCATCTTTCTTCATCTTTTAAGCCGGTTTCAATAACCTTCATCCTCTC 274
QY 23 ArgAspLeuThrSerSerSerSerAspGlnLeuSerTrpIleIleGlnLeuGluLys 42
DB 273 ACTCTCATCAGCAGCTTTTTCAGC-----TTCTTCCAGCTTTTGACAGGC 229
QY 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly---- 54
DB 228 AGTGGCCAGGCGCTCCCTGAGCAGGTCACGCTCTTTCACACGATGATCTCAGGTT 169
QY 55 -----ProPheAspGlnGlySerProPheAlaGlnLeuLeu 67
DB 168 CAAGAGGCCACCTCAGCCTCAGCCTGTCCCGGCGCCGCTTCTCCT-CAACTTCTC 110
QY 68 AspAspGlyGlnGlnAlaSerProTyrrHis-----ProGlySer 80
DB 109 GCTGGAGGCGCTCAGCTGCTCTCTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 50
QY 81 CysGlyAla 83
DB 49 TGGCGCTTCA 41
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RESULT 12

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US-09-667-857-139/C
; Sequence 139, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(521)
; OTHER INFORMATION: n = A,T,C or G
US-09-667-857-139
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Alignment Scores:

Pred. No.:	0.425	Length:	521
Score:	72.00	Matches:	31
Percent Similarity:	39.81%	Conservative:	10
Best Local Similarity:	30.10%	Mismatches:	32
Query Match:	16.18%	Indels:	31
DB:	4	Gaps:	5

US-08-978-217-7 (1-84) x US-09-667-857-139 (1-521)

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QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
DB 333 GAGTTCATCTTTCTTCATCTTTTAAGCCGGTTTCAATAACCTTCATCCTCTC 274
QY 23 ArgAspLeuThrSerSerSerSerAspGlnLeuSerTrpIleIleGlnLeuGluLys 42
DB 273 ACTCTCATCAGCAGCTTTTTCAGC-----TTCTTCCAGCTTTTGACAGGC 229
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QY 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly--- 54
DB 228 AGTGGCCAGGCGCTCCCTGAGCAGGTCACGCTCTTTCACACGATGATCTCAGGTT 169
QY 55 -----ProPheAspGlnGlySerProPheAlaGlnLeuLeu 67
DB 168 CAAGAGGCCACCTCAGCCTCAGCCTGTCCCGGCGCCGCTTCTCCT-CAACTTCTC 110
QY 68 AspAspGlyGlnGlnAlaSerProTyrrHis-----ProGlySer 80
DB 109 GCTGGAGGCGCTCAGCTGCTCTCTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 50
QY 81 CysGlyAla 83
DB 49 TGGCGCTTCA 41
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RESULT 13

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US-09-404-879A-92/C
; Sequence 92, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 92
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-92
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Alignment Scores:

Pred. No.:	0.46	Length:	551
Score:	72.00	Matches:	31
Percent Similarity:	39.81%	Conservative:	10
Best Local Similarity:	30.10%	Mismatches:	32
Query Match:	16.18%	Indels:	31
DB:	4	Gaps:	5

US-08-978-217-7 (1-84) x US-09-404-879A-92 (1-551)

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QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
DB 354 GAGTTCATCTTTCTTCATCTTTTAAGCCGGTTTCAATAACCTTCATCCTCTC 295
QY 23 ArgAspLeuThrSerSerSerSerAspGlnLeuSerTrpIleIleGlnLeuGluLys 42
DB 294 ACTCTCATCAGCAGCTTTTTCAGC-----TTCTTCCAGCTTTTGACAGGC 250
QY 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly--- 54
DB 249 AGTGGCCAGGCGCTCCCTGAGCAGGTCACGCTCTTTCACACGATGATCTCAGGTT 190
QY 55 -----ProPheAspGlnGlySerProPheAlaGlnLeuLeu 67
DB 189 CAAGAGGCCACCTCAGCCTCAGCCTGTCCCGGCGCCGCTTCTCCT-CAACTTCTC 131
QY 68 AspAspGlyGlnGlnAlaSerProTyrrHis-----ProGlySer 80
DB 130 GCTGGAGGCGCTCAGCTGCTCTCTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCT 71
QY 81 CysGlyAla 83
DB 70 TGGCGCTTCA 62
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RESULT 14
US-09-338-933-92/C

; Sequence 92, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 92
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-338-933-92

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Score: 72.00 Matches: 31
Percent Similarity: 39.81% Conservative: 10
Best Local Similarity: 30.10% Mismatches: 32
Query Match: 16.18% Indels: 31
DB: 4 Gaps: 5

US-08-978-217-7 (1-84) x US-09-338-933-92 (1-551)

QY 6 GlnLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
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QY 23 ArgAspLeuThrSerSerSerSerAspGlnLeuSerTrpIleIleGlnLeuGlnLeu 42
DB 294 ACTCTCATCAGCAGCTTTTTCAGC-----TTCTTCCAGCTTTTGCAGGGC 250
QY 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly--- 54
DB 249 AGTGGCCAGCGCCTCCTGACACGGTCCAGCTCTTCTTCAACAGCTGGATCTACGGTT 190
QY 55 -----ProPheAspGlnGlySerProPheAlaGlnLeuLeu 67
DB 189 CAAGAGGCCACCTCAGCTCAGCTGTCTCCGGCCCGCTTCTCCCT-CAACTTCTC 131
QY 68 AspAspGlyGlnGlnAlaSerProTrpHis-----ProGlySer 80
DB 130 GCTGAGGGCGCTCAGCTCGCTCCTGCAATCATCTGCTGCTGCTGCAAGAACTGGATCT 71
QY 81 CysGlyAla 83
DB 70 TGGCGTTCA 62

RESULT 15
US-09-215-681-92/c

; Sequence 92, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Frudakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215,681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 92
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-215-681-92

Alignment Scores:
Pred. No.: 0.46 Length: 551
Score: 72.00 Matches: 31
Percent Similarity: 39.81% Conservative: 10
Best Local Similarity: 30.10% Mismatches: 32
Query Match: 16.18% Indels: 31
DB: 4 Gaps: 5

US-08-978-217-7 (1-84) x US-09-215-681-92 (1-551)

QY 6 GlnLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
DB 354 GAGTTCATCTTTCTTCATCTTTTAAGCCCGGTTTCAATTAACCTTACCTCTCTC 295
QY 23 ArgAspLeuThrSerSerSerSerAspGlnLeuSerTrpIleIleGlnLeuGlnLeu 42
DB 294 ACTCTCATCAGCAGCTTTTTCAGC-----TTCTTCCAGCTTTTGCAGGGC 250
QY 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly--- 54
DB 249 AGTGGCCAGCGCCTCCTGACACGGTCCAGCTCTTCTTCAACAGCTGGATCTACGGTT 190
QY 55 -----ProPheAspGlnGlySerProPheAlaGlnLeuLeu 67
DB 189 CAAGAGGCCACCTCAGCTCAGCTGTCTCCGGCCCGCTTCTCCCT-CAACTTCTC 131
QY 68 AspAspGlyGlnGlnAlaSerProTrpHis-----ProGlySer 80
DB 130 GCTGAGGGCGCTCAGCTCGCTCCTGCAATCATCTGCTGCTGCTGCAAGAACTGGATCT 71
QY 81 CysGlyAla 83
DB 70 TGGCGTTCA 62

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Job time : 29.9382 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Gapop 10.0, Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications_NA:*

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- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	252	100.0	563	9	US-09-833-263-944
C 3	252	100.0	563	13	US-10-025-380-944
C 4	252	100.0	626	9	US-09-922-217-853
C 5	252	100.0	626	9	US-09-833-263-853
C 6	252	100.0	626	13	US-10-025-380-853
C 7	252	100.0	1907	14	US-10-097-340-74
C 8	252	100.0	1907	15	US-10-291-808-27
C 9	252	100.0	1915	9	US-09-964-824A-101
C 10	252	100.0	1915	9	US-09-964-824A-563
C 11	252	100.0	1915	9	US-09-880-107-3420
C 12	252	100.0	1915	9	US-09-967-768A-192

13	252	100.0	1917	9	US-09-922-217-1105	Sequence 1105, Ap
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15	252	100.0	1956	16	US-10-264-049-756	Sequence 756, Ap
16	252	100.0	1996	9	US-09-925-301-207	Sequence 207, Ap
17	252	100.0	2269	15	US-10-131-410-64	Sequence 64, Ap
18	249	98.8	355	9	US-09-867-701-4818	Sequence 4818, Ap
C 19	174	69.0	437	9	US-09-998-598-1740	Sequence 1740, Ap
C 20	63	25.0	437	9	US-09-998-598-2216	Sequence 2216, Ap
C 21	42.4	16.8	14538	17	US-10-741-601-49	Sequence 49, Ap
22	42.4	16.8	14745	17	US-10-741-601-48	Sequence 48, Ap
C 23	42	16.7	1286	17	US-10-437-963-38286	Sequence 38286, A
24	42	16.7	49680	16	US-10-459-262A-1	Sequence 1, Ap
25	40.4	16.0	13635	16	US-10-464-368-30	Sequence 30, Ap
26	40.4	16.0	13635	16	US-10-210-175-13	Sequence 13, Ap
27	40.4	16.0	13836	13	US-10-087-192-671	Sequence 671, Ap
28	40.4	16.0	14887	16	US-10-276-774-373	Sequence 373, Ap
29	40.4	16.0	14889	15	US-10-101-510-356	Sequence 356, Ap
30	40.4	16.0	14896	11	US-09-750-972-6	Sequence 6, Ap
C 31	40.4	16.0	14896	16	US-10-159-563-206	Sequence 206, Ap
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C 33	39	15.5	910	18	US-10-425-115-31177	Sequence 31177, A
34	38.8	15.4	532	13	US-10-027-632-280565	Sequence 280565, A
35	38.8	15.4	532	15	US-10-027-632-280565	Sequence 280565, A
36	38.8	15.4	534	15	US-10-023-386-25041	Sequence 25041, A
37	38.8	15.4	1011	15	US-10-023-386-25041	Sequence 3355, Ap
C 38	38.8	15.4	5173	9	US-09-880-107-3356	Sequence 1355, Ap
C 39	38.8	15.4	5173	15	US-10-171-581-159	Sequence 280564, A
40	38.4	15.2	532	13	US-10-027-632-280564	Sequence 280564, A
41	38.4	15.2	532	15	US-10-027-632-280564	Sequence 1461, Ap
42	38.2	15.2	201	17	US-10-741-601-1461	Sequence 1461, Ap
43	38.2	15.2	201	17	US-10-741-601-1504	Sequence 1504, A
44	38.2	15.2	946	17	US-10-437-963-53331	Sequence 53331, A
45	37.4	14.8	31263	16	US-10-282-122A-25447	Sequence 25447, A

ALIGNMENTS

RESULT 1
US-09-922-217-944/C
Sequence 944, Application US/09922217
Patent No. US200200764141
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeline Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongrong
APPLICANT: Jiang, Yuguin
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922, 217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 944
LENGTH: 563
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-217-944

Query Match 100.0%; Score 252; DB 9; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.7e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CAGCTGGAGACCTCACTTCAGCTCTTGTGATGAGCTCAAGTGGATTTAGAGCTGCTG 120
Db 412 CAGCTGGAGACCTCACTTCAGCTCTTGTGATGAGCTCAAGTGGATTTAGAGCTGCTG 353
QY 121 GAGAAGATGGATGGCTCTTCAAGAGGCTTAGACCCAGGCTCTTGAACAGGAGC 180
Db 352 GAGAAGATGGATGGCTCTTCAAGAGGCTTAGACCCAGGCTCTTGAACAGGAGC 293
QY 181 CCCTTTGCCAGAGCTGCTGAGAGGCTCAGAGGCTCAGAGGCTCTTGAACAGGAGC 240
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RESULT 2

US-09-833-944/c

Sequence 944, Application US/09833263

Patent No. US20020110547A1

GENERAL INFORMATION:

APPLICANT: Wang, Aijun

APPLICANT: Clapper, Jonathan D.

APPLICANT: Stolk, John A.

APPLICANT: Meagher, Madeleine J.

TITLE OF INVENTION: COMPOUNDS OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471C12

CURRENT APPLICATION NUMBER: US/09/833,263

CURRENT FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 944

LENGTH: 563

TYPE: DNA

ORGANISM: Homo sapien

US-09-833-263-944

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Query Match 100.0%; Score 252; DB 9; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.7e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CAGCTGGAGACCTCACTTCAGCTCTTGTGATGAGCTCAAGTGGATTTAGAGCTGCTG 120
Db 412 CAGCTGGAGACCTCACTTCAGCTCTTGTGATGAGCTCAAGTGGATTTAGAGCTGCTG 353
QY 121 GAGAAGATGGATGGCTCTTCAAGAGGCTTAGACCCAGGCTCTTGAACAGGAGC 180
Db 352 GAGAAGATGGATGGCTCTTCAAGAGGCTTAGACCCAGGCTCTTGAACAGGAGC 293
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Db 292 CCCTTTGCCAGAGCTGCTGAGAGGCTCAGAGGCTCAGAGGCTCTTGAACAGGAGC 233
QY 241 TGTGGCGCAGGA 252
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RESULT 3

US-10-025-380-944/c

Sequence 944, Application US/10025380

Publication No. US20020182191A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

```

APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skelky, Yashir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 944
LENGTH: 563
TYPE: DNA
ORGANISM: Homo sapiens
US-10-025-380-944

```

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Query Match 100.0%; Score 252; DB 13; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.7e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AATTGTCCTTGAGAGCTGCGCTCTTGGGCTCTGAGGAGCAACTCCATGCC 60
Db 472 AATTGTCCTTGAGAGCTGCGCTCTTGGGCTCTGAGGAGCAACTCCATGCC 413
QY 61 CAGCTGGAGACCTCACTTCAGCTCTTGTGATGAGCTCAAGTGGATTTAGAGCTGCTG 120
Db 412 CAGCTGGAGACCTCACTTCAGCTCTTGTGATGAGCTCAAGTGGATTTAGAGCTGCTG 353
QY 121 GAGAAGATGGATGGCTCTTCAAGAGGCTTAGACCCAGGCTCTTGAACAGGAGC 180
Db 352 GAGAAGATGGATGGCTCTTCAAGAGGCTTAGACCCAGGCTCTTGAACAGGAGC 293
QY 181 CCCTTTGCCAGAGCTGCTGAGAGGCTCAGAGGCTCAGAGGCTCTTGAACAGGAGC 240
Db 292 CCCTTTGCCAGAGCTGCTGAGAGGCTCAGAGGCTCAGAGGCTCTTGAACAGGAGC 233
QY 241 TGTGGCGCAGGA 252
Db 232 TGTGGCGCAGGA 221

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RESULT 4

US-09-922-217-853/c

Sequence 853, Application US/09922217

Patent No. US2002007641A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Lodes, Michael J.

APPLICANT: Secrist, Heather

APPLICANT: Benson, Darin R.

APPLICANT: Meagher, Madeleine Joy

APPLICANT: Stolk, John A.

APPLICANT: Wang, Tongtong

APPLICANT: Jiang, Yugu

APPLICANT: Smith, Carole Lynn

APPLICANT: King, Gordon E.

APPLICANT: Fanger, Jonathan D.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

FILE REFERENCE: 210121.471C13

;; CURRENT APPLICATION NUMBER: US/09/922,217
;; CURRENT FILING DATE: 2001-08-03
;; NUMBER OF SEQ ID NOS: 1124
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 853
;; LENGTH: 626
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-922-217-853

Query Match 100.0%; Score 252; DB 9; Length 626;
Best Local Similarity 100.0%; Pred. No. 2.8e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTGTCCTTTAGAGAGCTGCTGCTGCTTTGGGCTTTGGGGAGCCAACTCCATGCC 60
DB 471 AATTGTCCTTTAGAGAGCTGCTGCTGCTTTGGGCTTTGGGGAGCCAACTCCATGCC 412
QY 61 CAGCTGAGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGAGCTGCTG 120
DB 411 CAGCTGAGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGAGCTGCTG 352
QY 121 GAGAGAGATGAGATGAGCTTCCAGAGAGCCCTTAGACCCAGGCGCTTTGACAGGCGAGC 180
DB 351 GAGAGAGATGAGATGAGCTTCCAGAGAGCCCTTAGACCCAGGCGCTTTGACAGGCGAGC 292
QY 181 CCTTTGGCCAGAGAGCTGCTGAGACAGAGGTGACAGACCCCTTACCCAGCCCGGCGAGC 240
DB 291 CCTTTGGCCAGAGAGCTGCTGAGACAGAGGTGACAGACCCCTTACCCAGCCCGGCGAGC 232
QY 241 TGTGGCGCAGGA 252
DB 231 TGTGGCGCAGGA 220

RESULT 5

US-09-833-263-853/c
;; Sequence 853, Application US/09833263
;; Patent No. US20020110547A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Aijun
;; APPLICANT: Clapper, Jonathan D.
;; APPLICANT: Stolk, John A.
;; APPLICANT: Meagher, Madeleine J.
;; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
;; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
;; FILE REFERENCE: 210121.471C12
;; CURRENT APPLICATION NUMBER: US/09/833,263
;; CURRENT FILING DATE: 2001-04-10
;; NUMBER OF SEQ ID NOS: 1093
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 853
;; LENGTH: 626
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-833-263-853

Query Match 100.0%; Score 252; DB 9; Length 626;
Best Local Similarity 100.0%; Pred. No. 2.8e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTGTCCTTTAGAGAGCTGCTGCTGCTTTGGGCTTTGGGGAGCCAACTCCATGCC 60
DB 471 AATTGTCCTTTAGAGAGCTGCTGCTGCTTTGGGCTTTGGGGAGCCAACTCCATGCC 412
QY 61 CAGCTGAGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGAGCTGCTG 120
DB 411 CAGCTGAGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGAGCTGCTG 352
QY 121 GAGAGAGATGAGATGAGCTTCCAGAGAGCCCTTAGACCCAGGCGCTTTGACAGGCGAGC 180
DB 351 GAGAGAGATGAGATGAGCTTCCAGAGAGCCCTTAGACCCAGGCGCTTTGACAGGCGAGC 292

QY 181 CCTTTGGCCAGAGAGCTGCTGAGACAGGTGACAGACCCCTTACCCAGCCCGGCGAGC 240
DB 291 CCTTTGGCCAGAGAGCTGCTGAGACAGGTGACAGACCCCTTACCCAGCCCGGCGAGC 232
QY 241 TGTGGCGCAGGA 252
DB 231 TGTGGCGCAGGA 220

RESULT 6

US-10-025-380-853/c
;; Sequence 853, Application US/10025380
;; Publication No. US20020182191A1
;; GENERAL INFORMATION:
;; APPLICANT: Xu, Jiangchun
;; APPLICANT: Lodes, Michael J.
;; APPLICANT: Secrist, Heather
;; APPLICANT: Benson, Darin R.
;; APPLICANT: Meagher, Madeleine Joy
;; APPLICANT: Stolk, John A.
;; APPLICANT: Wang, Tongrong
;; APPLICANT: Jiang, Yugu
;; APPLICANT: Smith, Carole L.
;; APPLICANT: King, Gordon E.
;; APPLICANT: Wang, Aijun
;; APPLICANT: Clapper, Jonathan D.
;; APPLICANT: Skeiky, Yasir A. W.
;; APPLICANT: Fanger, Gary R.
;; APPLICANT: Vedvick Thomas S.
;; APPLICANT: Carter, Darick
;; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
;; FILE REFERENCE: 210121.471C14
;; CURRENT APPLICATION NUMBER: US/10/025,380
;; CURRENT FILING DATE: 2001-12-19
;; NUMBER OF SEQ ID NOS: 1129
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 853
;; LENGTH: 626
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-025-380-853

Query Match 100.0%; Score 252; DB 13; Length 626;
Best Local Similarity 100.0%; Pred. No. 2.8e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTGTCCTTTAGAGAGCTGCTGCTGCTTTGGGCTTTGGGGAGCCAACTCCATGCC 60
DB 471 AATTGTCCTTTAGAGAGCTGCTGCTGCTTTGGGCTTTGGGGAGCCAACTCCATGCC 412
QY 61 CAGCTGAGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGAGCTGCTG 120
DB 411 CAGCTGAGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGAGCTGCTG 352
QY 121 GAGAGAGATGAGATGAGCTTCCAGAGAGCCCTTAGACCCAGGCGCTTTGACAGGCGAGC 180
DB 351 GAGAGAGATGAGATGAGCTTCCAGAGAGCCCTTAGACCCAGGCGCTTTGACAGGCGAGC 292
QY 181 CCTTTGGCCAGAGAGCTGCTGAGACAGGTGACAGACCCCTTACCCAGCCCGGCGAGC 240
DB 291 CCTTTGGCCAGAGAGCTGCTGAGACAGGTGACAGACCCCTTACCCAGCCCGGCGAGC 232
QY 241 TGTGGCGCAGGA 252
DB 231 TGTGGCGCAGGA 220

RESULT 7

US-10-097-340-74
;; Sequence 74, Application US/10097340
;; Publication No. US20030087250A1
;; GENERAL INFORMATION:

```
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCHE
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VERIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy Of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 74
LENGTH: 1907
TYPE: DNA
ORGANISM: Homo sapiens
US-10-097-340-74
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Query Match 100.0%; Score 252; DB 14; Length 1907;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AATTGTCCTTGAAGAGCTGCTGCTCTTTGGGCTCTGGGGGACCACTCCATGCC 60
DB 405 AATTGTCCTTGAAGAGCTGCTGCTCTTTGGGCTCTGGGGGACCACTCCATGCC 464
QY 61 CAGCTGCGAGACCTCACTTCACAGCTCTTGTGATGAGCTCAAGTGGATGAGCTGCTG 120
DB 465 CAGCTGCGAGACCTCACTTCACAGCTCTTGTGATGAGCTCAAGTGGATGAGCTGCTG 524
QY 121 GAGAAGATGAGTGGCTTCCAGAGAGCCCTAGACCCAGAGCCCTTGAACAGGCGAGC 180
DB 525 GAGAAGATGAGTGGCTTCCAGAGAGCCCTAGACCCAGAGCCCTTGAACAGGCGAGC 584
QY 181 CCCTTTGCCAGAGCTGCTGAGAGAGCTCAAGAGCCCTTGAACAGGCGAGC 240
DB 585 CCCTTTGCCAGAGCTGCTGAGAGAGCTCAAGAGCCCTTGAACAGGCGAGC 644
QY 241 TGTGGCGCAGGA 252
DB 645 TGTGGCGCAGGA 656
```

```
RESULT 8
US-10-291-808-27
Sequence 27, Application US/10291808
Publication No. US20030224382A1
GENERAL INFORMATION:
```

```
APPLICANT: McClelland, Michael
APPLICANT: Welsh, John
APPLICANT: Trenkle, Thomas
TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
TITLE OF INVENTION: Using Same
FILE REFERENCE: F-PH 3457
CURRENT APPLICATION NUMBER: US/10/291,808
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: US/09/300,958
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/098,070
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/118,624
PRIOR FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 1907
TYPE: DNA
ORGANISM: Homo sapiens
US-10-291-808-27
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Query Match 100.0%; Score 252; DB 15; Length 1907;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AATTGTCCTTGAAGAGCTGCTGCTCTTTGGGCTCTGGGGGACCACTCCATGCC 60
DB 405 AATTGTCCTTGAAGAGCTGCTGCTCTTTGGGCTCTGGGGGACCACTCCATGCC 464
QY 61 CAGCTGCGAGACCTCACTTCACAGCTCTTGTGATGAGCTCAAGTGGATGAGCTGCTG 120
DB 465 CAGCTGCGAGACCTCACTTCACAGCTCTTGTGATGAGCTCAAGTGGATGAGCTGCTG 524
QY 121 GAGAAGATGAGTGGCTTCCAGAGAGCCCTAGACCCAGAGCCCTTGAACAGGCGAGC 180
DB 525 GAGAAGATGAGTGGCTTCCAGAGAGCCCTAGACCCAGAGCCCTTGAACAGGCGAGC 584
QY 181 CCCTTTGCCAGAGCTGCTGAGAGAGCTCAAGAGCCCTTGAACAGGCGAGC 240
DB 585 CCCTTTGCCAGAGCTGCTGAGAGAGCTCAAGAGCCCTTGAACAGGCGAGC 644
QY 241 TGTGGCGCAGGA 252
DB 645 TGTGGCGCAGGA 656
```

```
RESULT 9
US-09-964-824A-101
Sequence 101, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:
APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: Patentin version 3.0
SEQ ID NO 101
LENGTH: 1915
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-824A-101
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Query Match 100.0%; Score 252; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTGTCCTTGAAGAGCTGCTGTGCTTCTTGGGCTTGGGGGACCAACTCCATGCC 60
DB 429 AATTGTCCTTGAAGAGCTGCTGTGCTTCTTGGGCTTGGGGGACCAACTCCATGCC 488
QY 61 CAGCTCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGCTGCTG 120
DB 489 CAGCTCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGCTGCTG 548
QY 121 GAGAAGATGAGTGGCTTCCAGAGAGCCCTTAGACCCAGAGCCCTTTGACAGGGCAGC 180
DB 549 GAGAAGATGAGTGGCTTCCAGAGAGCCCTTAGACCCAGAGCCCTTTGACAGGGCAGC 608
QY 181 CCCTTTGCCAGAGCTGTGAGAGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGAGC 240
DB 609 CCCTTTGCCAGAGCTGTGAGAGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGAGC 668
QY 241 TGTGGCCGACGA 252
DB 669 TGTGGCCGACGA 680

RESULT 10
US-09-964-824A-563
Sequence 563, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:
APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: PatentIn version 3.0
SEQ ID NO 563
LENGTH: 1915
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-824A-563

Query Match 100.0%; Score 252; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTGTCCTTGAAGAGCTGCTGTGCTTCTTGGGCTTGGGGGACCAACTCCATGCC 60
DB 429 AATTGTCCTTGAAGAGCTGCTGTGCTTCTTGGGCTTGGGGGACCAACTCCATGCC 488
QY 61 CAGCTCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGCTGCTG 120
DB 489 CAGCTCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGCTGCTG 548
QY 121 GAGAAGATGAGTGGCTTCCAGAGAGCCCTTAGACCCAGAGCCCTTTGACAGGGCAGC 180
DB 549 GAGAAGATGAGTGGCTTCCAGAGAGCCCTTAGACCCAGAGCCCTTTGACAGGGCAGC 608
QY 181 CCCTTTGCCAGAGCTGTGAGAGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGAGC 240
DB 609 CCCTTTGCCAGAGCTGTGAGAGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGAGC 668
QY 241 TGTGGCCGACGA 252
DB 669 TGTGGCCGACGA 680

DB 669 TGTGGCCGACGA 680

RESULT 11
US-09-880-107-3420
Sequence 3420, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3420
LENGTH: 1915
TYPE: DNA
ORGANISM: Homo sapiens
OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843
US-09-880-107-3420

Query Match 100.0%; Score 252; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTGTCCTTGAAGAGCTGCTGTGCTTCTTGGGCTTGGGGGACCAACTCCATGCC 60
DB 429 AATTGTCCTTGAAGAGCTGCTGTGCTTCTTGGGCTTGGGGGACCAACTCCATGCC 488
QY 61 CAGCTCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGCTGCTG 120
DB 489 CAGCTCGAGACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTTAGCTGCTG 548
QY 121 GAGAAGATGAGTGGCTTCCAGAGAGCCCTTAGACCCAGAGCCCTTTGACAGGGCAGC 180
DB 549 GAGAAGATGAGTGGCTTCCAGAGAGCCCTTAGACCCAGAGCCCTTTGACAGGGCAGC 608
QY 181 CCCTTTGCCAGAGCTGTGAGAGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGAGC 240
DB 609 CCCTTTGCCAGAGCTGTGAGAGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGAGC 668
QY 241 TGTGGCCGACGA 252
DB 669 TGTGGCCGACGA 680

RESULT 12
US-09-967-768A-192
Sequence 192, Application US/09967768A
Patent No. US20020150877A1
GENERAL INFORMATION:
APPLICANT: Augstus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325

SOFTWARE: PatentIn version 3.0
; SEQ ID NO 192
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-192

Query Match 100.0%; Score 252; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTGTCCTTGAAGAGCTGCGCTCTTGGGCTCTGGGGGACCAATTCATGCC 60
DB 429 AATTGTCCTTGAAGAGCTGCGCTCTTGGGCTCTGGGGGACCAATTCATGCC 488
QY 61 CAGCTCGAGAACCTTCACTTCCAGTCTTGTGATGAGCTGAGTATGATGAGCTGCTG 120
DB 489 CAGCTCGAGAACCTTCACTTCCAGTCTTGTGATGAGCTGAGTATGATGAGCTGCTG 548
QY 121 GAGAGGATGGAGTGGCTTCCAGAGAGCCCTAGACCCAGGGCCCTTGAACAGGGCAGC 180
DB 549 GAGAGGATGGAGTGGCTTCCAGAGAGCCCTAGACCCAGGGCCCTTGAACAGGGCAGC 608
QY 181 CCCTTTGCCAGAGAGTGTCTGAGACGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGGCAGC 240
DB 609 CCCTTTGCCAGAGAGTGTCTGAGACGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGGCAGC 668
QY 241 TGTGGCGCAGGA 252
DB 669 TGTGGCGCAGGA 680

RESULT 13

US-09-922-217-1105
; Sequence 1105, Application US/09922217
; Patent No. US2002007641A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aljun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922.217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-1105

Query Match 100.0%; Score 252; DB 9; Length 1917;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTGTCCTTGAAGAGCTGCGCTCTTGGGCTCTGGGGGACCAATTCATGCC 60
DB 431 AATTGTCCTTGAAGAGCTGCGCTCTTGGGCTCTGGGGGACCAATTCATGCC 490
QY 61 CAGCTCGAGAACCTTCACTTCCAGTCTTGTGATGAGCTGAGTATGATGAGCTGCTG 120
DB 491 CAGCTCGAGAACCTTCACTTCCAGTCTTGTGATGAGCTGAGTATGATGAGCTGCTG 550

QY 121 GAGAGGATGGAGTGGCTTCCAGAGAGCCCTAGACCCAGGGCCCTTTGACCAAGGCGAGC 180
DB 551 GAGAGGATGGAGTGGCTTCCAGAGAGCCCTAGACCCAGGGCCCTTTGACCAAGGCGAGC 610
QY 181 CCCTTTGCCAGAGAGTGTCTGAGACGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGGCAGC 240
DB 611 CCCTTTGCCAGAGAGTGTCTGAGACGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGGCAGC 670

QY 241 TGTGGCGCAGGA 252
DB 671 TGTGGCGCAGGA 682

RESULT 14

US-10-025-380-1105
; Sequence 1105, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aljun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-1105

Query Match 100.0%; Score 252; DB 13; Length 1917;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTGTCCTTGAAGAGCTGCGCTCTTGGGCTCTGGGGGACCAATTCATGCC 60
DB 431 AATTGTCCTTGAAGAGCTGCGCTCTTGGGCTCTGGGGGACCAATTCATGCC 490
QY 61 CAGCTCGAGAACCTTCACTTCCAGTCTTGTGATGAGCTGAGTATGATGAGCTGCTG 120
DB 491 CAGCTCGAGAACCTTCACTTCCAGTCTTGTGATGAGCTGAGTATGATGAGCTGCTG 550
QY 121 GAGAGGATGGAGTGGCTTCCAGAGAGCCCTAGACCCAGGGCCCTTGAACAGGGCAGC 180
DB 551 GAGAGGATGGAGTGGCTTCCAGAGAGCCCTAGACCCAGGGCCCTTGAACAGGGCAGC 610
QY 181 CCCTTTGCCAGAGAGTGTCTGAGACGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGGCAGC 240
DB 611 CCCTTTGCCAGAGAGTGTCTGAGACGAGCTCAGCAAGCCCAAGCCCTTACCAAGCCGGCAGC 670
QY 241 TGTGGCGCAGGA 252
DB 671 TGTGGCGCAGGA 682

RESULT 15
US-10-264-049-756
; Sequence 756, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 756
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-049-756

Query Match 100.0%; Score 252; DB 16; Length 1956;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AATTGGCCCTTGAGAGCTGCGTCTTGTGCTTTGGGCTCTGGGGACCACTCCATGCC	60
Db	470	AATTGGCCCTTGAGAGCTGCGTCTTGTGCTTTGGGCTCTGGGGACCACTCCATGCC	529
QY	61	CAGCTGGAGAGCTCACTTCCAGCTCTTGTATGAGCTCAGTTGATCATTGAGCTGCTG	120
Db	530	CAGCTGGAGAGCTCACTTCCAGCTCTTGTATGAGCTCAGTTGATCATTGAGCTGCTG	589
QY	121	GAGAAGGATGGCATGCGCTTCCAGAGGCCCTTAGACCCAGGGCCCTTTGACCAAGGCAGC	180
Db	590	GAGAAGGATGGCATGCGCTTCCAGAGGCCCTTAGACCCAGGGCCCTTTGACCAAGGCAGC	649
QY	181	CCCTTTGCCAGAGAGCTGCTGAGAGAGTCAAGCAAGCCCTTACCAACCCCGGAGC	240
Db	650	CCCTTTGCCAGAGAGCTGCTGAGAGAGTCAAGCAAGCCCTTACCAACCCCGGAGC	709
QY	241	TGTGGCGCAGGA	252
Db	710	TGTGGCGCAGGA	721

Search completed: November 15, 2004, 23:08:41
Job time : 121.189 secs

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:35:22 ; Search time 21.2888 Seconds
(without alignments)
8413.757 Million cell updates/sec

Title: US-08-978-217-6

Perfect score: 252

Sequence: 1 AATTGGCCCTTGAGGAGCT.....CCGACAGCTGTGGCGCAGGA 252

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1643014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	DB ID	Description
1	252	100.0	1907 4 US-09-300-958A-27	Sequence 27, Appl
2	252	100.0	1907 4 US-09-570-593-4	Sequence 4, Appl
3	252	100.0	1920 1 US-08-746-789A-1	Sequence 1, Appl
4	39	15.5	276 4 US-09-313-294A-3437	Sequence 3437, Ap
5	38.8	15.4	5173 1 US-08-242-677-1	Sequence 1, Appl
6	36.2	14.4	741 4 US-09-252-991A-12066	Sequence 12066, A
7	36.2	14.4	918 4 US-09-252-991A-12009	Sequence 12009, A
8	36.2	14.4	1650 4 US-09-252-991A-8097	Sequence 8097, Ap
9	36.2	14.4	2145 4 US-09-252-991A-8205	Sequence 8205, Ap
10	35	13.9	1975 2 US-08-852-743-1	Sequence 1, Appl
11	35	13.9	1975 3 US-09-185-370-1	Sequence 1, Appl
12	35	13.9	2161 2 US-08-712-709-4	Sequence 4, Appl
13	35	13.9	2161 3 US-09-111-444-4	Sequence 4, Appl
14	35	13.9	2161 4 US-09-541-228-4	Sequence 4, Appl
15	34.8	13.8	621 4 US-09-252-991A-8781	Sequence 8781, Ap
16	34.8	13.8	921 4 US-09-252-991A-9092	Sequence 9092, Ap
17	34.8	13.8	1512 4 US-09-252-991A-9180	Sequence 9180, Ap
18	34.8	13.8	1533 4 US-09-252-991A-8895	Sequence 8895, Ap
19	34.8	13.8	1758 4 US-09-252-991A-8997	Sequence 8997, Ap
20	34.6	13.7	6972 4 US-09-595-684B-38	Sequence 38, Appl
21	34.6	13.7	8309 4 US-09-620-312D-1083	Sequence 1083, Ap
22	34.4	13.7	780 4 US-09-489-039A-4778	Sequence 4778, Ap
23	34	13.5	3141 2 US-08-956-242-1	Sequence 1, Appl
24	34	13.5	3141 3 US-09-351-215-1	Sequence 1, Appl
25	33.8	13.4	2128 4 US-09-620-312D-197	Sequence 197, Appl
26	33.8	13.4	25603 4 US-09-819-607-3	Sequence 3, Appl
27	33.6	13.3	465 4 US-09-621-976-2488	Sequence 2488, Ap

28	33.6	13.3	618 4 US-09-252-991A-7654	Sequence 7654, Ap
29	33.6	13.3	687 4 US-09-780-717-30	Sequence 30, Appl
30	33.6	13.3	744 4 US-09-252-991A-7749	Sequence 7749, Appl
31	33.6	13.3	798 4 US-09-252-991A-7739	Sequence 7739, Appl
32	33.6	13.3	1214 4 US-09-780-717-28	Sequence 28, Appl
33	33.4	13.3	4970 4 US-09-816-095-1	Sequence 1, Appl
34	33.2	13.2	921 4 US-09-252-991A-1415	Sequence 1415, Ap
35	33.2	13.2	1206 4 US-09-252-991A-16406	Sequence 16406, A
36	33.2	13.2	1983 4 US-09-252-991A-16300	Sequence 16300, A
37	33	13.1	1107 4 US-09-252-991A-3936	Sequence 3936, Ap
38	33	13.1	1134 4 US-09-252-991A-3908	Sequence 3908, Ap
39	33	13.1	1217 3 US-09-594-669-11	Sequence 11, Appl
40	33	13.1	1217 3 US-10-112-432-11	Sequence 11, Appl
41	33	13.1	1304 3 US-09-594-669-9	Sequence 9, Appl
42	33	13.1	1304 4 US-10-112-432-9	Sequence 9, Appl
43	33	13.1	1326 4 US-09-252-991A-4002	Sequence 4002, Ap
44	33	13.1	1420 3 US-09-594-669-7	Sequence 7, Appl
45	33	13.1	1421 4 US-10-112-432-7	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-09-300-958A-27
; Sequence 27, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McCrelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR FILING DATE: 1998-04-27
; PRIOR FILING DATE: 1998-08-27
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-27

Query Match      100.0%; Score 252; DB 4; Length 1907;
Best Local Similarity 100.0%; Pred. No. 3.9e-60;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AATTGGCCCTTGAGGAGCTGCTGCTCTTGGGCTCTGAGGAGCACTCCATGCC 60
DB      |||
QY      405 AATTGGCCCTTGAGGAGCTGCTGCTCTTGGGCTCTGAGGAGCACTCCATGCC 464
DB      |||
QY      61 CAGCTCGAGACCTCACTTCCAGCTCTTGTGATGAGCTCAGTTGATCTTGAAGCTGCTG 120
DB      |||
QY      465 CAGCTCGAGACCTCACTTCCAGCTCTTGTGATGAGCTCAGTTGATCTTGAAGCTGCTG 524
DB      |||
QY      121 GAGAAAGATGGCAGTGGCTCTTCCAGAGGCGCTTGAAGCTCCTTTTGAAGAGGCTGCTG 180
DB      |||
QY      525 GAGAAAGATGGCAGTGGCTCTTCCAGAGGCGCTTGAAGCTCCTTTTGAAGAGGCTGCTG 584
DB      |||
QY      181 CCCTTTGCCAGAGCTGCTGAGCAGGCTTCAAGAGCCAGCCCTTACACCCGCGGAGC 240
DB      |||
QY      585 CCCTTTGCCAGAGCTGCTGAGCAGGCTTCAAGAGCCAGCCCTTACACCCGCGGAGC 644
DB      |||
QY      241 TGTGGCGCAGGA 252
DB      |||
QY      645 TGTGGCGCAGGA 656
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RESULT 2
US-09-570-593-4
; Sequence 4, Application US/09570593
; Patent No. 6566063
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Harrowe, Greg
; TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 2300-1556
; CURRENT APPLICATION NUMBER: US/09/570,593
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1211)
; OTHER INFORMATION: Human epithelial-restricted with serine box (ESX)
; OTHER INFORMATION: protein.
US-09-570-593-4

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Query Match Similarity      100.0%; Score 252; DB 4; Length 1907;
Best Local Similarity      100.0%; Pred. No 3.9e-60;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 AATTGTGCGCCCTTGAGAGAGCTGCGTCTGTGCTTTTGTGGCCCTCTGGGGGAGCAACACTCCATGCG 60
DB      405 AATTGTGCGCCCTTGAGAGAGCTGCGTCTGTGCTTTTGTGGCCCTCTGGGGGAGCAACACTCCATGCG 464
QY      61 CAGCTGGGAGAGACTTCACTTCCAGCTCTTTCTATATGAGCTCAGTTGATCATTTAGCTGCTG 120
DB      465 CAGCTGGGAGAGACTTCACTTCCAGCTCTTTCTATATGAGCTCAGTTGATCATTTAGCTGCTG 524
QY      121 GAGAAAGATGAGCATGAGCCTCTTCAGGAGGCGCTTAGACCCAGGCGCCCTTTGACAGGAGGACAGC 180
DB      525 GAGAAAGATGAGCATGAGCCTCTTCAGGAGGCGCTTAGACCCAGGCGCCCTTTGACAGGAGGACAGC 584
QY      181 CCCCTTGGCCCGAGAGCTGCTGAGCGACGCTCAGCAAGCCAGCCCTTACCACTCCCGGACAGC 240
DB      585 CCCCTTGGCCCGAGAGCTGCTGAGCGACGCTCAGCAAGCCAGCCCTTACCACTCCCGGACAGC 644
QY      241 TGTGCGCGCAGGA 252
DB      645 TGTGCGCGCAGGA 656

RESULT 3
US-08-746-789A-1
; Sequence 1, Application us/08746789A
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismail Kola, Martin J. Tymms, Christine Debouck
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member. EUP3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486

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1 OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
2 SOFTWARE: MICROSOFT WORD
3
4 CURRENT APPLICATION DATA:
5 APPLICATION NUMBER: US/08/746,789A
6 FILING DATE: No. 5789200ember 15, 1996
7 CLASSIFICATION: 514
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER:
10 FILING DATE:
11 ATTORNEY/AGENT INFORMATION:
12 NAME: William T. Han
13 REGISTRATION NUMBER: 34,344
14 REFERENCE/DOCKET NUMBER: ATG 50024
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 610 270 5219
17 TELEFAX: 610 270 4026
18 INFORMATION FOR SEQ ID NO: 1:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 1920
21 TYPE: Nucleic Acid
22 STRANDEDNESS: Single
23 TOPOLOGY: Linear
24 ANTI-SENSE: No
25
26 US-08-746-789A-1

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Query Match	100.0%	Score 252	DB 1	Length 1920
Best Local Similarity	100.0%	Prod. No. 3	9e-60	
Matches 252	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	1	AATTGTGCGCTTGAAGAGCTGCGTGTGCTCTTTGGGCGCTCTGGGGAGCAACTCCATCC	60	
Db	424	AATTGTGCGCTTGAAGAGCTGCGTGTGCTCTTTGGGCGCTCTGGGGAGCAACTCCATCC	483	
OY	61	CAGCTGGAGACCTCACTTCAGCTCTTCTGATAGCTCAGTTGGATCATGAGCTGCTG	120	
Db	484	CAGCTGGAGACCTCACTTCAGCTCTTCTGATAGCTCAGTTGGATCATGAGCTGCTG	543	
OY	121	GAGAAAGATGGCATGCGCTTCCAGAGGCGCTTAAGCCAGGGCGCTTTGACCAAGGCGAGC	180	
Db	544	GAGAAAGATGGCATGCGCTTCCAGAGGCGCTTCAAGAACCCAGGCGCTTTGACCAAGGCGAGC	603	
OY	181	CCCTTTGCCCGAGAGCTGCTGGAAGAGGATCAGCAAGCGACCCCTCAACACCCGGCGAGC	240	
Db	604	CCCTTTGCCCGAGAGCTGCTGGAAGAGGATCAGCAAGCGACCCCTCAACACCCGGCGAGC	663	
OY	241	TGTGGCGCGAGCA	252	
Db	664	TGTGGCGCGAGCA	675	

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RESULT 4
US-09-313-294A-3437
; Sequence 3437, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ico, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OR INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ. ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 3437
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700611585H1
US-09-313-294A-3437

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Query Match 15.5%; Score 39; DB 4; Length 276;
Best Local Similarity 49.3%; Pred. No. 0.081;
Matches 102; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 42 GGGGACCACTGATGAGCCAGCTGAGACCTTCACTTCCAGCTTTTGATAGCTCAG 101
DB 60 GGTGGAGCCACTGCTGAGGAGCTTCCGACGCTTCTCATTTCCGATCCGCTTCCC 119
QY 102 TTGATCATTTGATGCTGCTGAGAGATGAGCATGAGCTTCCAGAGGCTTACAGCCAG 161
DB 120 GCAGATCTGGAGATTTCTACAAGAGAGCGGTGGCTCTTCTTGACAGCGCCAGAGATTGA 179
QY 162 GCCCTTTGACAGAGGAGCCCTTTTGCCAGAGCTGCTGAGACGAGCTCAGAACCCAG 221
DB 180 CCTCTGCGCGAGCGCCCGGACCTGGAGAGGCGCTGTCCCCGACGAGGCGCATTTCAT 239
QY 222 CCCCTACACCCCGGAGCTGTGGCCG 248
DB 240 CTCTCACTGCTGCTGCTTCTTCCCGC 266

RESULT 5

US-08-242-677-1/c
; Sequence 1, Application US/08242677
; Patent No. 5677143
; GENERAL INFORMATION:
; APPLICANT: Gaynor, Richard B
; APPLICANT: Wu, Foon W.
; TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
; TITLE OF INVENTION: and uses thereof in regulating Gene Expression and in the
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,677
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5173 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4863
; US-08-242-677-1

Query Match 15.4%; Score 38.8; DB 1; Length 5173;
Best Local Similarity 50.5%; Pred. No. 0.21;
Matches 94; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 48 CCAACTGCATCCAGCTGCGAGACCTCACTTCAGCTTTGATGAGCTCAGTTGAT 107

DB 193 CCACTCGCGCCCGCTTCGGAGAGCCGCTGCGCCCGCTGCGCGGCTCTCTCT 134
QY 108 CATTGAGCTGTGAGAGATGAGCATGAGCTTTCAGAGAGGCTTGAACCCAGGCTT 167
DB 133 CTTGAGCGGCTGTGAGAGAGAGCGAGGCTTCCAGCGGCTTCCGGATGCTCCCTT 74
QY 168 TGAACGGGACGCGCTTTCAGAGAGCTGTGACAGAGGTCAAGAACCAAGCCCTTA 227
DB 73 GGCACAGCGCCCAAGACAGAGGCGCGGCTCCGCTGTGACAGAGCAGCGCTCCGCGA 14
QY 228 CCAACC 233
DB 13 GCACCC 8

RESULT 6

US-09-252-991A-12066
; Sequence 12066, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12066
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-12066

Query Match 14.4%; Score 36.2; DB 4; Length 741;
Best Local Similarity 47.6%; Pred. No. 0.62;
Matches 107; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 16 GAGCTGCGTGTGTCTTTGAGGCTTGGAGGACCACTTCATGCCAGCTGCGAGACTTC 75
DB 29 GAGCGCTTCTCGCGCGCGGAGCGGCTGGAACCTGGAACCTGCGCTGTGACTG 88
QY 76 ACTTCAAGCTTTTGTATGAGCTCACTGATTCATTTGAGTCTGGAAGAGATGCGATG 135
DB 89 AACACCACTTCATCAAGGCAATGATGACATCTGACTCTCGAAGAGGCCACAG 148
QY 136 GCCTTCAGAGAGGCTTACACCGAGGCGCTTGTGACAGAGGAGCCCTTGGCCAGAG 195
DB 149 GCGGCTGCGCGGTACGCTGCTGCGCTGCACTACAGCCGCGCAAGAGGCTGCGGAG 208
QY 196 CTGCTGAGAGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
DB 209 CTGGCGGAGAGGATTCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 253

RESULT 7

US-09-252-991A-12009
; Sequence 12009, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12009
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12009

Query Match 14.4%; Score 36.2; DB 4; Length 918;
Best Local Similarity 47.6%; Pred. No. 0.66;
Matches 107; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 16 GACCTGGTGTGCTTCTTGGGAGGAGCAATCCATGCGCCAGTCCGAGACTC 75
DB 676 GACGCTTCTTCCGCGGCGGAGCGGCGCTGGAAGTGAAGTCTGCTGTACTG 735
QY 76 ACTTCCAGCTCTTCTGATGAGCTCAGTTGATCATTGAGCTGCTGAGAGATGGCATG 135
DB 736 AACACCACTTGCATCAAGGCCATGATGACATCTTCACTGCTCGAAGAGGCCACACAG 735
QY 136 GCCTTCCAGAGAGGCGCTTAGACCCAGGCGCTTGAACGAGGAGCGCCCTTTGGCCAGAG 195
DB 796 GGGGCTGCGCGGCTGACCTGCGCTGACCTAGACGAGCGGCAACGAGGTGCGCGAG 855
QY 196 CTGCTGACGACGCTCAGCAAGCGCCCTTACCAACCGGCGAGC 240
DB 856 CTGCGCGAGAGGTTCGCGGAGACTGACGCTTCCCTTCCCATTC 900

RESULT 8
US-09-252-991A-8097/C
; Sequence 8097, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8097
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8097

Query Match 14.4%; Score 36.2; DB 4; Length 1650;
Best Local Similarity 47.9%; Pred. No. 0.78;
Matches 104; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 7 GCCCTTGAGAGCTGCTGCTGCTTCTTGGGAGGAGCAATCCATGCGCCAGCTG 66
DB 657 GGCATGATAGCGCGGCTGACCGCGGCGGAGTCTGCTGCTGACGACGAGCGCGGTTG 598
QY 67 CGAGACTCTACTTCCAGCTCTTCTGATGAGCTCAGTTGATTCATTGAGTCTGCTGAGAG 126
DB 597 CGAGCCCTGGGCGCGGCTCACCAGGAGTCTGCGCGGCGGAGGAGGCGGCGAA 538
QY 127 GATGAGATGCTCTTCCAGAGGCGCTTGAACGAGGCGCTTTGACGAGGAGCGCCCTTT 186
DB 537 GCGCAGGTGTGTTCGCGGCGGAGTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478
QY 187 GCCCAGAGCTGCTGAGCAAGCGGTGACCAAGCCAGCC 223
DB 477 CTGCTAGAGCAGCGGAGGAGACACAGCATGACTTCC 441

RESULT 9
US-09-252-991A-8205

; Sequence 8205, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8205
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8205

Query Match 14.4%; Score 36.2; DB 4; Length 2145;
Best Local Similarity 47.9%; Pred. No. 0.84;
Matches 104; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 7 GCCCTTGAGAGCTGCTGCTGCTTCTTGGGAGGAGCAATCCATGCGCCAGCTG 66
DB 1516 GGCATGATAGCGCGGCTGACCGCGGCGGAGTCTGCTGCTGACGACGAGCGCGGTTG 1575
QY 67 CGAGACTCTACTTCCAGCTCTTCTGATGAGCTCAGTTGATTCATTGAGTCTGCTGAGAG 126
DB 1576 CGAGCCCTGGGCGCGGCTGACCGCGGAGTCTGCGGCGGCGGAGGAGCGGCGGAA 1635
QY 127 GATGAGATGCTCTTCCAGAGGCGCTTGAACGAGGCGCTTTGACGAGGAGCGCCCTTT 186
DB 1636 GCGCAGGTGTGTTCGCGGCGGAGTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1695
QY 187 GCCCAGAGCTGCTGAGCAAGCGGTGACCAAGCCAGCC 223
DB 1696 CTGCTAGAGCAGCGGAGGAGACACAGCATGACTTCC 1732

RESULT 10
US-08-852-743-1
; Sequence 1, Application US/08852743
; Patent No. 5830699
; GENERAL INFORMATION:
; APPLICANT: Force, Thomas
; APPLICANT: Kyriakis, John M.
; APPLICANT: Pomo, Celia M.
; APPLICANT: Bonventure, Joseph
; TITLE OF INVENTION: SOK-1 AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,743
; FILING DATE: 7-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/016,774
; FILING DATE: 7-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/327001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 127...1404
US-08-852-743-1

Query Match 13.9%; Score 35; DB 2; Length 1975;
Best Local Similarity 48.3%; Pred. No. 1.7;
Matches 98; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 46 GACCACTCCATGCCAGCTGCGAGACCTTCAGCTCTTCTGATGAGCTCAGTTGG 105
DB 175 GAGGAGCTCTTCAACCAAGCTGACCGCATTTGGCAAGGCTCGTTGGGAGGCTTCAAG 234
QY 106 ATCATGAGCTGCTGAGAGATGATGCGCTTCCAGAGAGCCCTAGACCCAGGGCCC 165
DB 235 GCGATGATTAACACACAAAGAGGTGTGGCCATCAATCACTGAGAGAGGCC 294
QY 166 TTGACCAAGGAGCCCTTTGGCCAGAGCTGTCGAGCAGCGCTGAGAGAGGCC 225
DB 295 GAGGATGATGATGAGAGATCCAGAGATCACTGTCTCACTGATGTCGACAGCCCC 354
QY 226 TACCACCCCGCAGCTGTGGCGC 248
DB 355 TACATCACCGCTACTTGGCTC 377

RESULT 11
US-09-185-370-1
Sequence 1, Application US/09185370
Patent No. 6093560
GENERAL INFORMATION:
APPLICANT: Force, Thomas
APPLICANT: Kyriakis, John M.
APPLICANT: Pombo, Celia M.
APPLICANT: Bonventure, Joseph
TITLE OF INVENTION: SOK-1 AND METHODS OF USE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/185,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852,743
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/327001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 127...1404
US-09-185-370-1

Query Match 13.9%; Score 35; DB 3; Length 1975;
Best Local Similarity 48.3%; Pred. No. 1.7;
Matches 98; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 46 GACCACTCCATGCCAGCTGCGAGACCTTCAGCTCTTCTGATGAGCTCAGTTGG 105
DB 175 GAGGAGCTCTTCAACCAAGCTGACCGCATTTGGCAAGGCTCGTTGGGAGGCTTCAAG 234
QY 106 ATCATGAGCTGCTGAGAGATGATGCGCTTCCAGAGAGCCCTAGACCCAGGGCCC 165
DB 235 GCGATGATTAACACACAAAGAGGTGTGGCCATCAATCACTGAGAGAGGCC 294
QY 166 TTGACCAAGGAGCCCTTTGGCCAGAGCTGTCGAGCAGCGTCAAGAGCCAGGCC 225
DB 295 GAGGATGATGATGAGAGATCCAGAGATCACTGTCTCACTGATGTCGACAGCCCC 354
QY 226 TACCACCCCGCAGCTGTGGCGC 248
DB 355 TACATCACCGCTACTTGGCTC 377

RESULT 12
US-08-712-709-4
Sequence 4, Application US/08712709
Patent No. 5863780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-712-709-4

Query Match 13.9%; Score 35; DB 2; Length 2161;
Best Local Similarity 48.3%; Pred. No. 1.8;
Matches 98; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 46 GACCACTCCATGCCCCAGCTGCGAGACCTCACTTCAGCTCTTGATGAGCTGAGTTGG 105
DB 286 GAGAGAGCTCTTCAACCAAGCTCGACCGCATTTGGCAAGGCTCTGTTGGGAGAGTCTACAG 345
QY 106 ATGATTGAGCTGCTGAGAGAGATGCGATGGCCCTTCAGAGAGGCCCTAGACCCAGGGGCC 165
DB 346 GGCATCGATTAACCAACAAAGAGAGTGTGGCCATCAAGATCATCGACTGAGAGAGGCC 405
QY 166 TTGACCAAGGAGAGCCCTTTGGCCAGAGAGCTGCTGAGACGAGTCAAGCCAGGCCCC 225
DB 406 GAGGATGAGATCGAGACATCCAGCAGAGATCATCTCTCTCACTCAGTGCAGAGGCC 465
QY 226 TACCACCCCGGCACTGTGGCGC 248
DB 466 TACATCACCGCTACTTGGCTC 488

RESULT 13
US-09-111-444-4
Sequence 4, Application US/09111444
Patent No. 6045792

GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guebler, Karl U.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,444
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709

ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY:

CLONE: Consensus
US-09-111-444-4

Query Match 13.9%; Score 35; DB 3; Length 2161;
Best Local Similarity 48.3%; Pred. No. 1.8;
Matches 98; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 46 GACCACTCCATGCCCCAGCTGCGAGACCTCACTTCAGCTCTTGATGAGCTGAGTTGG 105
DB 286 GAGAGAGCTCTTCAACCAAGCTCGACCGCATTTGGCAAGGCTCTGTTGGGAGAGTCTACAG 345
QY 106 ATGATTGAGCTGCTGAGAGAGATGCGATGGCCCTTCAGAGAGGCCCTAGACCCAGGGGCC 165
DB 346 GGCATCGATTAACCAACAAAGAGAGTGTGGCCATCAAGATCATCGACTGAGAGAGGCC 405
QY 166 TTGACCAAGGAGAGCCCTTTGGCCAGAGAGCTGCTGAGACGAGTCAAGCCAGGCCCC 225
DB 406 GAGGATGAGATCGAGACATCCAGCAGAGATCATCTCTCTCACTCAGTGCAGAGGCC 465
QY 226 TACCACCCCGGCACTGTGGCGC 248
DB 466 TACATCACCGCTACTTGGCTC 488

RESULT 14
US-09-541-228-4
Sequence 4, Application US/09541228
Patent No. 6232077

GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guebler, Karl U.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/541,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709

ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-09-541-228-4

Query Match 13.9%; Score 35; DB 3; Length 2161;
Best Local Similarity 48.3%; Pred. No. 1.8;

Matches 98; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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QY 46 GACCACTCATGCGGCTGCGAGACCTTCCAGCTTCTGTGATGAGTCAAGTTGG 105
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Db 286 GAGGAGCTCTTCAACCAAGCTCGACCCGATTGGCAAGGGCTCGTTGGGAGGTCTTACAG 345
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QY 106 ATCATTGAGCTGCTGAGAGATGAGATGAGCCCTTCCAGAGAGCCCTAGACCCAGGGCCC 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 346 GGCATGATTAACACACAAAGAGAGTGTGGCCATCAAGATCATCGACTGAGAGAGGCC 405
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QY 166 TTGACCAAGGAGCCCTTTGCGCAGAGCTGCTGAGACGAGTCAGCAAGCCAGGCC 225
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Db 406 GAGGATGAGATCGAGACATCGACAGAGATCATGTCTCTCAGTCAGTGCGACAGGCC 465
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 226 TACCACCCCGCAGCTGTGGCC 248
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Db 466 TACATCACCGCTACTTGGCTC 488
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RESULT 15

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US-09-252-991A-8781/C
; Sequence 8781, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8781
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8781
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Query Match 13.8%; Score 34.8; DB 4; Length 621;

Best Local Similarity 54.8%; Pred. No. 1.4;

Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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QY 105 GATCATTTAGCTGCTGAGAGATGAGATGAGCCCTTCCAGAGAGCCCTAGACCCAGGGCC 164
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 576 GACCGCTGACCCGCTCGGCGAGGCGGCCGACGCGCTCCAGGTGCTCGATCCAGAGCA 517
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QY 165 CTTTGACCAAGGAGCCCTTTGCGCAGAGCTGCTGAGACGAGTCAGCAAGCCAGGCC 224
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Db 516 CGGTGAGCGCGCTGGCGCAGTCGACAGACAGCCGCTCGAAGACCTGATGCGGCCCT 457
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QY 225 CTACCA 230
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Db 456 CGTCGA 451
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Search completed: November 15, 2004, 14:14:01
Job time: 23.2888 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 21:57:02 ; Search time 624.355 Seconds
(without alignments)
3209.338 Million cell updates/sec

Title: US-08-978-217-2
Perfect score: 1980
Sequence: 1 MATCEISNIFSNFYSAWYS.....YKFKKNSGKKEEVLQSHN 371

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3625171 segs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO.spool_p/US08978217/runat_15112004_103133_12813/app_query.fasta_1.1500
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPEXCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human0.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=pcct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEASize=500 -MINLEN=0
-MXPEN=200000000 -USER=US08978217 @CGN_1_1_1189 @runat_15112004_103133_12813
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA: *
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19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq: *
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21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1980	100.0	1907	14	US-10-097-340-74
2	1980	100.0	1907	15	US-10-291-808-27
3	1980	100.0	1915	9	US-09-964-824A-101
4	1980	100.0	1915	9	US-09-964-824A-563
5	1980	100.0	1915	9	US-09-880-107-3420
6	1980	100.0	1915	9	US-09-667-768A-192
7	1980	100.0	1917	13	US-09-922-217-1105
8	1980	100.0	1917	13	US-10-025-380-1105
9	1980	100.0	1956	16	US-10-264-049-756
10	1980	100.0	1996	9	US-09-925-301-207
11	1654	83.5	2269	15	US-10-131-410-54
12	1127	56.9	626	9	US-09-922-217-853
13	1127	56.9	626	9	US-09-833-263-853
14	1127	56.9	626	13	US-10-025-380-853
15	1011	51.1	563	9	US-09-922-217-944
16	1011	51.1	563	9	US-09-833-263-944
17	1011	51.1	563	13	US-10-025-380-944
18	903	45.6	502	9	US-09-604-287A-282
19	903	45.6	502	9	US-09-834-759-282
20	903	45.6	502	9	US-09-339-338-282
21	903	45.6	502	10	US-09-551-621-282
22	903	45.6	502	13	US-10-007-805-282
23	903	45.6	502	14	US-10-076-622-282
24	903	45.6	502	15	US-10-124-805-282
25	822	41.5	499	9	US-09-998-598-2290
26	652	32.9	437	9	US-09-998-598-2216
27	618	31.2	355	9	US-09-867-701-4818
28	558	28.2	1429	9	US-09-764-864-320
29	556.5	28.1	1426	9	US-09-925-297-309
30	556.5	28.1	1426	15	US-10-106-698-935
31	554.5	28.0	1435	15	US-10-017-161-1953
32	554.5	28.0	1435	15	US-10-292-758-1601
33	519.5	26.2	852	9	US-09-759-143-44
34	519.5	26.2	852	9	US-09-780-665-44
35	519.5	26.2	852	9	US-09-030-606-44
36	519.5	26.2	852	9	US-09-822-827-44
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38	519.5	26.2	852	9	US-09-232-880-44
39	519.5	26.2	852	9	US-09-895-793-44
40	519.5	26.2	852	9	US-09-895-814-44
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43	519.5	26.2	852	15	US-10-144-678A-44
44	519.5	26.2	852	15	US-10-294-025-44
45	519.5	26.2	852	17	US-10-688-838-44

ALIGNMENTS

RESULT 1
US-10-097-340-74
; Sequence 74, Application US/10097340
; Publication No. US20030087250A1
GENERAL INFORMATION:
; APPLICANT: JOHN MONAHAN
; APPLICANT: Manjula GANNANARAPU
; APPLICANT: Sebastian HOERSCHE
; APPLICANT: Subhangai KAMATKAR
; APPLICANT: Steve G KOVARS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MITLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT

; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
 ; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
 ; FILE REFERENCE: MRI-030
 ; CURRENT APPLICATION NUMBER: US/10/097,340
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 60/276,025
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/325,149
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/276,026
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/324,967
 ; PRIOR FILING DATE: 2001/09/26
 ; PRIOR APPLICATION NUMBER: 60/311,732
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/325,102
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/323,580
 ; PRIOR FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 363
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 74
 ; LENGTH: 1907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-097-340-74

Alignment Scores:

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 Score: 1980.00 Matches: 371
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-08-978-217-2 (1-371) x US-10-097-340-74 (1-1907)

QY 1 MetAlaAlaThrCysGluIleSerAsnIlePheSerAsnTyrPheSerAlaMetTyrSer 20
 Db 96 ATGGCTGCAACCTGTGATAGCACTTTTATGCAACTTCACTGAGTGCATGAC 155
 QY 21 SerGluAspSerThrLeuAlaSerValProProAlaAlaThrPheGlyAlaAspAspLeu 40
 Db 156 TCGAGAGACTCCACCTGGCTCTGTTCCCTGCTCCACCTTGGGGCCGATGACTTG 215
 QY 41 ValLeuThrLeuSerAsnProGlnMetSerLeuGlnGlyThrGluValAspTyrPheLeu 60
 Db 216 GTACTGACCTGTAGCAACCCCAAGTGTCACTGAGGGTACAGAGAGGCGCAGCTGGTTG 275
 QY 61 GtGluGlnProGlnPheTyrSerTyrThrGlnValLeuAspTyrPheSerTyrGlnVal 80
 Db 276 GGGGAACAGCCCACTTCTGTGACAGACCGAGTTTGAATGATGATCACTCAAGTG 335
 QY 81 GluLysAsnLysTyrAspAlaSerAlaIleAspPheSerTyrCysAspMetAspGlyAla 100
 Db 336 GAGAGAAACAAGTACGACGCAAGGCGCATTTGCTCAAGATGTGATGATGGGCC 395
 QY 101 ThrLeuCysAsnCysAlaLeuGluLeuArgLeuValPheGlyProLeuGlyAspGln 120
 Db 396 ACCCTGTGCAATGTGCTTGTGAGAGACTGCTGTGCTTTGGGCTTGGGGGACCA 455
 QY 121 LeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTyrPheIle 140
 Db 456 CTCATGCCAGCTGCGAGACCTCACTTCCAGCTCTTCTATGATGATCACTTGGATCAT 515
 QY 141 GluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
 Db 516 GACGTCTGAGAGAGATGATGATGCTTCCAGAGGCGCTTAAAGCCAGGGCCCTTTGAC 575
 QY 161 GtGluGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis 180
 Db 576 CAGGGCAGCCCTTTGCTGCGAGAGCTGTGACGACGATGACGAGCAAGCCCTTACAC 635

QY 181 ProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
 Db 636 CCCGGCAGCTGTGCGCAGAGAGCCCCCTCCCTGGCAGCTTGAAGCTTCCACCGCAGGG 695
 QY 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp 220
 Db 696 ACTGGTCTTCTCGAGGCTCCCACTCTCAAGCTCGGAGGAGTGAAGTGAAGTGAAGTGA 755
 QY 221 ProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysLysGlyAspPro 240
 Db 756 CCCACTGATGCGAAGCTCTTCCCAAGCTGATTTTGTGATGCTGCAAGAGAGGGGATCCC 815
 QY 241 LysHisGlyLysArgLysArgLysArgProArgLysLeuSerLysGlyLysTyrTrpAspCys 260
 Db 816 AAGCAGCGGAGAGGAGAAAGAGGCGCGCCCGGAAAGCTGAGCAAGAGTGAAGTGAAGTGA 875
 QY 261 LeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrPheLysPheLeuArg 280
 Db 876 CTGAGGGGCAAGAGAGGAGCAGCGCCGAGGAGCAGCCACTGTGAGAGTTCATCCGG 935
 QY 281 AspIleLeuIleHisAspProGluLeuAsnGluGlyLeuMetLysTyrPheLysPheLysGlu 300
 Db 936 GACATCTCATTCACCCGAGCTCAACGAGGCTTATAGTGGAGAAATGGCATGAA 995
 QY 301 GlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTyrPheGlyGlnLysLys 320
 Db 996 GCGCTTCAAGTCTCTGGCTCCGAGGCTGTGAGGCCCACTATGGGCCCAAAAGAAAG 1055
 QY 321 AsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGlu 340
 Db 1056 AACAGCAACATGACCTTACAGAGAGCTGACCGGCGCATAGGATCACTACAAACCGGAG 1115
 QY 341 IleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSerGly 360
 Db 1116 ATCTGGAACGGGTGATGCGCGGCGCATCTGCTACAAAGTTTGGCAAAATCTCAAGCGGC 1175
 QY 361 TrpLysGluGluGluValLeuGlnSerArgAsn 371
 Db 1176 TGGAGAGAGAGAGGTTCTCCAGAGTCCGAAAC 1208

RESULT 2

; US-10-291-808-27
 ; Sequence 27, Application US/10291808
 ; Publication No. US20030224382A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCelland, Michael
 ; APPLICANT: Welsh, John
 ; APPLICANT: Tremler, Thomas
 ; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
 ; FILE REFERENCE: P-PH 3457
 ; CURRENT APPLICATION NUMBER: US/10/291,808
 ; CURRENT FILING DATE: 2002-11-07
 ; PRIOR APPLICATION NUMBER: US/09/300,958
 ; PRIOR FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: 60/083,331
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: 60/098,070
 ; PRIOR FILING DATE: 1998-08-27
 ; PRIOR APPLICATION NUMBER: 60/118,624
 ; PRIOR FILING DATE: 1999-02-04
 ; NUMBER OF SEQ ID NOS: 85
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 27
 ; LENGTH: 1907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-291-808-27

Alignment Scores:
 Pred. No.: 4,45e-219 Length: 1907
 Score: 1980.00 Matches: 371
 Percent Similarity: 100.00% Conservative: 0

Beet Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0
 US-08-978-217-2 (1-371) x US-10-291-808-27 (1-1907)

QY 1 MetalAlaThrCysGluIleSerAsnIlePheSerAsnIlePheSerAlaMetTyrSer 20
 DB ATGGCTGCAACCTGTGATGATTACCACTTTTAGCACTCTCACTGCGATGAC 155

QY 21 SerGluAspSerThrLeuAlaSerValProProAlaAlaThrPheGluAlaAspAspLeu 40
 DB TCGAGGAGCTCCACCTGGCTGTGTCCCTGCTGCGACCTTTGGGGCGGATGACTTG 215

QY 41 ValLeuThrLeuSerAsnProGlnMetSerLeuGluGlyThrGluIleValAspTyrPhe 60
 DB GATCTACCTGAGCAACCCCGAGATGCTATGAGAGGTACAGAGAGGCGACCTGTTG 275

QY 61 GlyGluGlnProGlnPheTyrSerIleThrGlnValLeuAspTyrIleSerTyrGlnVal 80
 DB GGGGAAACAGCCCGAGTTCTGTGTGAGAGCGCAGCTTGTGATCGATCGACTACAGTG 335

QY 81 GluIleAsnIleTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAspGlyAla 100
 DB GAGAGAACAGATGACGACGCGCATTTGATCTCAAGATGTGACATGATGAGCGCC 395

QY 101 ThrLeuCysAsnCysAlaLeuGluGluIleValPheGlyProLeuGluIleAspGln 120
 DB ACCCTCTGCAATGTGTGCTGAGAGCTGCTGTGCTTGTGCTGCTGCTGCTGCTGCTG 455

QY 121 LeuHISAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTyrIleIle 140
 DB CTCACGCTCCAGCTGCGAGCTCCTCACTTCCAGCTCTTCTGATAGCTCAGATTGATCAT 515

QY 141 GluLeuLeuGluIleIleAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
 DB GAGCTGCTGAGAGAGATGCGATGCTTCCAGAGGCGCTTACAGCCAGGCGCTTGTGAC 575

QY 161 GlnGlySerProPheAlaGlnGluIleLeuAspAspGlyGlnGlnAlaSerProTyrHis 180
 DB CAGGAGGAGCCCTTGTGCTGAGAGCTGCTGAGAGCTGAGAGGCGACCCCTTACAC 635

QY 181 ProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
 DB CCGGAGAGCTGTGCGAGAGAGCCCTTCCCTGCGAGCTTCAAGCTTCTCAACGCGAG 655

QY 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp 220
 DB ACTGAGCTTCTCGAGAGCTCCACTCTCAGACTCCGCTGAGAGTACGTCGAGACTGAT 755

QY 221 ProThrAspGlyIleIlePheProSerAspGlyPheArgAspCysIleValAspPro 240
 DB CCCACCTGATGCGAGAGCTTCCCGAGAGTGTTCGTGATGCTGCAAGAGGCGGATCCC 815

QY 241 LysHISGlyIleAspArgIleArgProArgIleIleLeuSerIleGlyTyrTyrAspCys 260
 DB AACGAGGAGAGGAGAGAGAGGCGGCGCCCGAGAGCTGAGCAAGATCTGAGAGCTGT 875

QY 261 LeuGluGlyIleIleAspSerIleValAlaProArgGlyThrHisLeuTyrGlnPheIleArg 280
 DB CTGAGAGGAG 935

QY 281 AspIleLeuIleHisProGluLeuAsnGluGlyLeuMetIleTyrGlnAlaGlnHisGln 300
 DB GACATCTCTCAACAG 995

QY 301 GlyValPheIleAspSerArgSerGluAlaValAlaGlnLeuTyrPheGlyIleValIle 320
 DB GGGGCTTCAAGTCTTCCGCTGCGAGAGCTGTGCGCCCAATGAGGCGCAAGAGAGAG 1055

QY 321 AsnSerAsnMetThrTyrGluIleIleSerArgAlaMetArgTyrTyrIleValGln 340
 DB AACGAG 1115

QY 341 IleLeuGluArgValAspGlyArgArgLeuValTyrIlePheGlyIleAsnSerSerGly 360
 DB ATCTCGAAGAGGCTGATGATGCGGCGAGCTCTCAAGATTTGGCAAAACTCAAGCGGC 1175

QY 361 TrpIleGluGluGluValLeuGlnSerArgAsn 371
 DB TGGAG 1208

RESULT 3
 US-09-964-824A-101
 ; Sequence 101, Application US/09964824A
 ; Patent No. US20020102531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horitzan, Stephen
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
 ; TITLE OF INVENTION: Set
 ; FILE REFERENCE: 689290-73
 ; CURRENT APPLICATION NUMBER: US/09/964,824A
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US/60/236,033
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236,032
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236,028
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 583
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 101
 ; LENGTH: 1915
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-964-824A-101

Alignment Scores:
 Pred. No.: 4,47e-219 Length: 1915
 Score: 1980.00 Matches: 371
 Percent Similarity: 100.00% Conservative: 0
 Beet Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-08-978-217-2 (1-371) x US-09-964-824A-101 (1-1915)

QY 1 MetalAlaThrCysGluIleSerAsnIlePheSerAsnIlePheSerAlaMetTyrSer 20
 DB ATGGCTGCAACCTGTGATGATTACCACTTTTAGCACTCTCACTGCGATGAC 179

QY 21 SerGluAspSerThrLeuAlaSerValProProAlaAlaThrPheGlyAlaAspAspLeu 40
 DB TCGAGGAGCTCCACCTGGCTGTGTCCCTGCTGCGACCTTTGGGGCGGATGACTTG 239

QY 41 ValLeuThrLeuSerAsnProGlnMetSerLeuGluGlyThrGluIleValAspTyrPhe 60
 DB GATCTACCTGAGCAACCCCGAGATGCTATGAGAGGTACAGAGAGGCGACCTGTTG 299

QY 61 GlyGluGlnProGlnPheTyrSerIleThrGlnValLeuAspTyrIleSerTyrGlnVal 80
 DB GGGGAAACAGCCCGAGTTCTGTGTGAGAGCGCAGGTTCTGAGATGATGATCAAGAGTG 359

QY 81 GluIleAsnIleTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAspGlyAla 100
 DB GAGAGAACAGATGACGACGCGCATTTGATCTCAAGATGTGACATGATGAGCGCC 419

QY 101 ThrLeuCysAsnCysAlaLeuGluGluIleValPheGlyProLeuGluIleAspGln 120
 DB ACCCTCTGCAATGTGTGCTGAGAGCTGCTGTGCTTGTGCTGCTGCTGCTGCTGCTG 479

QY 121 LeuHISAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTyrIleIle 140
 DB CTCACGCTCCAGCTGCGAGCTCCTCACTTCCAGCTCTTCTGATAGCTCAGATTGATCAT 539

QY 141 GluLeuLeuGluIleIleAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160

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Db      540 GACCTGCTGAGAGAGATGCGATGCGCTTCAGAGAGCCCTAGACCCAGGCGCCCTTGAC
Qy      161 GtHGlSerProPhaElaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis
Db      600 CAGGAGAGCCCTTTGCGAGAGACTCTTGAGAGACGCTGAGAGAGCCAGCCCTTACAC
Qy      181 ProGlySerCyGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly
Db      660 CCGGAGAGCTGTGGCGGAGAGGCCCTCCCTCGGAGAGCTGAGCGTCTCACCGGAGGG
Qy      201 ThnGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp
Db      720 ACTGAGGCTTCTCGAGACTCCCACTCTCAAGACTCCCGTGAAGTGAAGTGAAGTGAAGT
Qy      221 ProThrAspGlyLeuLeuPheProSerAspGlyPheArgAspCysValSerGlyAspPro
Db      780 CCACTGATGAGAGAGCTTCTCCAGGAGTGTCTTCTGATGAGAGAGAGGAGATCCC
Qy      241 LysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyLysTyrAspCys
Db      840 AAGCAGCGGAGAGGAGAAACGAGGCGGCGCCGAAAGCTGAGCAAGAGTACTGGAGCTGT
Qy      261 LeuGlyGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrGlnPheLeuArg
Db      900 CTCGAGGCGGAGAGAGCAAGCAAGCGCCGCAAGGCAAGCCTGTGGAGTTCATCCGG
Qy      281 AspGlyLeuLeuHisAspProGlyLeuAspGlyGlyLeuMetLysTyrGlnAsnArgHisGly
Db      960 GAGATCTCTCAAGTCCAGCCGAGGCTTCAGAGAGGCTCTAGAGAGTGGAGAGTGGCATGAA
Qy      301 GlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTyrGlnLysLysLys
Db      1020 GGGGTCTTCAAGTTCCTGGGCTCGAGGCTGTGGCCCACTATGGGGCCAAAAGAAAG
Qy      321 AsnSerAsnMetThrTyrGlyLysLeuSerArgAlaMetCysTyrTyrTyrLysArgGly
Db      1080 AACAGCAACATGACCTTACGAGAGCTGAGCGGGCCATGAGTACTACTCAACACGGGAG
Qy      341 IleLeuGlnArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSerGly
Db      1140 ATCTGAGAGCGGTGATGAGCGGCGAGCTGTCTCAAGATTGGCAAAACTCAAGCGGC
Qy      361 TrpLysGlyGlnGlyValLeuGlnSerArgAsn
Db      1200 TGGAGAGGAGAGGTTCTCCAGAGTCCGAGAC 1232

RESULT 4
US-09-964-824A-563
; Sequence 563, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 563
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-563

```

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Pred. No.: 4,47e-219 Length: 1915
Score: 1980.00 Matches: 371
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-978-217-2 (1-371) x US-09-964-824A-563 (1-1915)
Qy      1 MetAlaAlaThrCysGlnLysSerAsnIlePheSerAsnTyrPheSerAlaMetCysTyr
Db      120 ATGGCTGCAACTGTGATGATTAGCAACATTTTATGAACTACTTCACTGATGATGATGATGAT
Qy      21 SerGlyAspSerThrLeuAlaSerValProProAlaAlaThrPheGlyAlaAspLeu
Db      180 TCGAGAGACTCCACCTTGAGCTCTGTCTCCCTGCTGACCACTTTGGGCGGATGATCTTG
Qy      41 ValLeuThrLeuSerAsnProGlnMetSerLeuGlnGlyThrGlyLysAlaSerTrpLeu
Db      240 GATCTGACCTTGAGCAACCCCGAGATGATGAGAGGATGAGAGAGGAGGAGGAGGAGGAGG
Qy      61 GlyGlnGlnProGlnPheTyrPheTyrSerLysThrGlnValLeuAspTrpLysTyrGlnVal
Db      300 GGGGAGACGCCCCAGTTCCTGTGAGAGAGCCAGTTCGATGATGATGATGATGATGATGATG
Qy      81 GlyLysAsnLysTyrAsnAlaSerAlaIleAspPheSerArgCysAspMetAspGlyAla
Db      360 GAGAGACAGAGTACGACGCAAGCCGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      101 ThrLeuCysAsnCysAlaLeuGlnGlyLeuValPheGlyProLeuGlyAspGln
Db      420 ACCCTCTGCAATTTGTGCCCTTGAAGAGCTGCTGTGCTTTTGGGCTTGAGGAGGAGGAGG
Qy      121 LeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGlyLeuSerTrpLysLeu
Db      480 CTTCATGCCAGCTGCGAGAGCTCACTTCAAGCTCTTCTGATGAGCTCACTTGGATGAT
Qy      141 GlnLeuLeuGlnLysAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyProPheAsp
Db      540 GAGCTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
Qy      161 GlnGlySerProPheAlaGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis
Db      600 CAGGAGAGCCCTTTGGCCAGAGCTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG
Qy      181 ProGlySerCyGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly
Db      660 CCGGAGAGCTGTGGCGGAGAGGCCCTCCCTCGGAGAGCTGTGAGCTCTCCACCGAGGG
Qy      201 ThnGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp
Db      720 ACTGAGGCTTCTCGAGACTCCCACTCTCAGACTCGGAGTGAAGTGAAGTGAAGTGAAGT
Qy      221 ProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysValSerGlyAspPro
Db      780 CCACTGATGAGAGAGCTTCTCCAGGAGTGTCTTCTGATGAGAGAGAGGAGGAGATCCC
Qy      241 LysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyLysTyrAspCys
Db      840 AAGCAGCGGAGAGGAGAAACGAGGCGGCGCCGAAAGCTGAGCAAGAGTACTGGAGCTGT
Qy      261 LeuGlyGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrGlnPheLeuArg
Db      900 CTCGAGGCGGAGAGAGCAAGCAAGCGCCGCAAGGCAAGCCTGTGGAGTTCATCCGG
Qy      281 AspGlyLeuLeuHisAspProGlyLeuAspGlyGlyLeuMetLysTyrGlnAsnArgHisGly
Db      960 GAGATCTCTCAAGTCCAGCCGAGGCTTCAGAGAGGCTCTAGAGAGTGGAGAGATGAGCATGAA
Qy      301 GlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTyrGlnLysLysLys
Db      1020 GGGGTCTTCAAGTTCCTGGGCTCGAGGCTGTGGCCCACTATGGGGCCAAAAGAAAG 1079

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< Alignment Scores:

Qy	Db	Qy	Db	Qy	Db	Qy	Db
321	1080	341	1140	361	1200	371	1232
tsnserAamctTrrYgLiLlysenserAgaIamcAcgYrrYrrYrYsarggiu	AACGCAACATGACTTACGAGAGCTGAGCCGGCCATGAGGACTTACTACAAACGGAGG	IleleugIuaGrvaIaSPGIYAgrgrheuValTYrrYsPhegILYsAsnserSercily	ATCTCGAACGGGTGAGTGGCCGGCGACTCGTCTTCAAGATTGGCAAAACTCAAGCGGC	TrplysGIugIuIuaIleuGIInserAraAsn	TGGAAGAGAGAAAGGTTCTCTCAAGATCGGAAC		

RESULT 5

Sequence 4420, Application/us/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Iwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-MO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3420
LENGTH: 1915
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843
US-09-880-107-3420

Alignment Scores:

Pred. No.:	4,476-219	1915
Score:	1880.00	371
Percent Similarity:	100.00%	0
Best Local Similarity:	100.00%	0
Query Match:	100.00%	0
Indels:		0
Gaps:		0
DB:	9	

US-08-978-217-2 (1-371) x US-09-880-107-3420 (1-1915)

QY	1	MetAlaAlaThrCysGluIleSerSerAnIlePheSerAnIleTyrPheSerAlaMetTyrSer	20
Db	120	ATGGCTGCACCACTGTAGATTAGCAACATTTTTCACCACTCTCATGGCGCATTTACAGC	179
QY	21	SerGluAspSerThrIleuAlaSerValProProlAlaIatThrPheGluValaAspAspLeu	40
Db	180	TGGAGAGACTCACCTGGCCTCTGTTCCTCCCTGCTGCACACTTTGGGACCGAAGACTTG	239
QY	41	ValIeuThrIleuSerAnPProGlnMetSerIleuGluGlyThrGluValaSerTyrLeu	60
Db	240	GTACTGACCTGAGCAACCCCAAGTGTATTGGAGGGTACAGAAAGCGACGCTGGTTG	299
QY	61	GlyGluGlnProGlnPheThrPheTyrSerIlyThrGlnValIleuAspTyrPLeuTyrGlnVal	80
Db	300	GGGGAACAGCCCACTGTCTGTCTGAAGCGCAGGTTTGCATGGATCATGACCAAGTG	359
QY	81	GluIlyAsnIlyTyrAspAlaSerAlaIleAlaPheSerAArgCysAspMetAspGlyVala	100
Db	360	GAGAAAGAACAGTACACCAACCGCATTCCTCACATGTGATGATGGATGGGGCC	419
QY	101	ThrIleuCybAnCysValaIleuGluGluIleuAlaGluValaPheGlyProLeuGluAlaAspGln	120
Db	420	ACCCTCTGCATATGTCCCTTGAAGAGCTCGCTGTGGTCTTTTGGGCTCTTGGGAGACCA	479

OY	121	LeuHisIaIaGlnLeuAaGAspLeuThrSerSerSerSerAspGluLeuSerTrpIaIle	140
Db	480	CTCAATGCCCAAGCTCGCAAGACTACTTCCAGCTCTTCTGATAGCTCAAGTGGATCAATT	539
OY	141	GluLeuLeuGluIuYAspGlyMeValaPheGlnGlnIuIaLeuAspProGlyProPheAsp	160
Db	540	GAGCTGCTGAGGAAGATGGCATGGCTTCCAGAGAGGCCCTTAGACCCAGGGGCTTTGAC	599
OY	161	GlnGlySerProPheIaIaGlnGlnLeuLeuAspAspGlyGlnGlnIaIaSerProTyrHis	180
Db	600	CAGGGACAGCCCCCTTGGCCAGAGACTCTGACACACGTCAGCAAGCAGGCCCTTACAC	659
OY	181	ProGlySerCysGlyIaIaGlyValaProSerProGlySerSerAspValaSerThrAlaGly	200
Db	660	CCCCGACACTGTGGCGCAGAGAGCCCCCTCCCTGGACACTTGAACGTCTCCACCGCAGGG	719
OY	201	ThrGlyIaAsaAaGSerSerHisIaSerSerAspSerGlyGlySerAspValaAspLeuAsp	220
Db	720	ACTGATGCTTCTCGGAGCTCCCACTCTCAAGACTCCGATGGAGTGAAGTGAAGCTTGAT	779
OY	221	ProThrAspGlyValaLeuPheProSerAspGlyPheAspAspCysGlyValaAspPro	240
Db	780	CCCACTGATGGCAAGCTCTTCCCAAGAGATGGTTTGTGACTGCAAGAAAGGGGGAATCCC	839
OY	241	LyHisIaGlyLyAsGlyLyAsGlyLyAsArgProArgLyLeuSerLyGlyIuTyrTrpAspCys	260
Db	840	AAGACACGGGAGACGGAAACAAGGCCGGGCCCGAAGACTGACACAAAGATCTGGGACTGT	899
OY	261	LeuGlnGlyLyLySAserLyHisIaIaProArgGlyThrHisLeuTrpGluPheIaArg	280
Db	900	CTCGAGGGCAAGAGAGAGACGAGCGCCGACGAGGACCCCACTGTGGAGATTCAATCCGG	959
OY	281	AspIleLeuIleHisProGlnLeuLeuAsnGlnGlyLeuMetLystrpGluAsnArgHisGln	300
Db	960	GACATCTCTCAATCCACCCGAGACTCAACAGAGGGCTCTGAAGTGGGGAATCCGCATGAA	1019
OY	301	GlyValaPheLyPheLeuAaGSerSerGlyValaValaIaGlnLeuTrpGlyGlnLyLeuSAs	320
Db	1020	GGGCTCTTCAAGTTCTCTGGCGTCCGAGGCTGTGGCCCACTATGGGGCCAAAAGAAAAG	1079
OY	321	AsnSerAsnMetThrTyrGlnLyLeuLeuSerArgIaMetArgTyrTyrLyAsArgIu	340
Db	1080	AACAGCAACATGACCTACAGAGAACTGAGCGGGCCATGAGGTACTACTCAAAACGGGAG	1139
OY	341	IleLeuGluArgValaAspGlyArgArgLeuValTyrLyPheGlyLyAsnSerSerGly	360
Db	1140	ATCTCTGGAACGGGTGATGGCCCGGCACTGCTCAACAAGTTTGCAAAAACCTCAAGCGGC	1199
OY	361	TrpLyAsGlnGluIuValaIleuGlnSerArgAsn	371
Db	1200	TGAAAGAGAGAGAGGTTCTTCCAAAGTCCGGAAC	1232

RESULT

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US-09-967-768A--192
; Sequence 192, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 192
; LENGTH: 1915

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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-967-768A-192

Alignment Scores:
  pred. No.:      4,47e-219      Length:      1915
  Score:          1980.00         Matches:      371
  Percent Similarity: 100.00%     Conservative: 0
  Best Local Similarity: 100.00%   Mismatches:  0
  Query Match:    100.00%         Indels:      0
  DB:              9              Gaps:          0

US-08-978-217-2 (1-371) x US-09-967-768A-192 (1-1915)

QY      1 MetAlaAlaThrcysglulleserAnllepheserAntyrPheSerAlaMetTySer 20
Db      120 ATGGCTGCACCTGTGAGATTAGCAACATTTTAGCACTTCACTGAGTGAAGC 179

QY      21 SerGluAspSerThrleuAlaSerValProProAlaAlaThrPheGlyAlaAspAspLeu 40
Db      180 TCGGAGACTCCACCCCTGGCTCTGTTCCCTCTGCTCCACCTTTGGGGCCGATGACTTG 239

QY      41 ValLeuThrleuSerAspProGlnMetSerleuGluGlyThrGluValAspAspLeu 60
Db      240 GATCTGACCTTGAGCAACCCCAAGATGCTATGGAGGGTACAGAAAGGCGAGCTGGTGG 239

QY      61 GlyGluGlnProGlnPheTrpSerlyThrGlnValLeuAspTrpIleSerTyrglnVal 80
Db      300 GGGGAACAGCCCAAGTTCTGTGTAAGACCAAGGTTTGACAGTGGATGCCAAGTG 359

QY      81 GluLysAsnLysTyrrAspAlaSerAlaIleAspPheSerArgCysAspMetAspGlyAla 100
Db      360 GAGAGAAACAATGACGACGCAAGGCCATGACTTCTCAGATGTGACATGATGGGCC 419

QY      101 ThrleuCysAsnCysAlaLeuGluGluLeuArgLeuValPheGlyProleuGlyAspGln 120
Db      420 ACCCTCTGCATTTGCTTGTGAGAGCTGCTGTGCTTGTGGCTCTGGGGAGACAA 479

QY      121 LeuHisAlaGlnleuArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIle 140
Db      480 CTCATGACCCAGCTGGAGACCTCCTCAGCTTCTGATGAGCTCACTTGATGAT 539

QY      141 GluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
Db      540 GACCTGCTGAGAGAGATGCGATGCGCTTCAGAGGCCCTTAGACCCAGGCCCTTTGAC 599

QY      161 GlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnIleAspProGlyHis 180
Db      600 CAGGGACGCCCTTTGCCAGAGCTGCTGAGACGCTGACAGCAAGCCACCTTACAC 659

QY      181 ProGlySerCysgllyalaglyAlaProSerProGlySerSerAspValSerThrAlaGly 200
Db      660 CCGGGAGCTGTGGCGGAGAGGCCCTCCCTCGGAGCTCTGACGCTCCACCGGAGGG 719

QY      201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp 220
Db      720 ACTGGCTCTCTCTCGAGCTCCCACTCTCAGACTCCCGTGAAGTGACTGTGACCTGGAT 779

QY      221 ProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysLysGlyAspPro 240
Db      780 CCACTGATGGCAAGCTCTTCCCAAGGATGTTTCTGATCTGCAAGAAAGGGGATCCC 839

QY      241 LysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTrpTrpAspCys 260
Db      840 AACCAAGGAGGAGGAGAAAGAGGCGCGCCGCAAGTGAAGCAAAAGTACTGGACTGT 899

QY      261 LeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArg 280
Db      900 CTCGAGGGGCAAGAGCAAGCAAGCGCCCAAGAGGCAACCACTGTGGGAGTTTCACTCCGG 959

QY      281 ArgGlyLeuLeuHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGlu 300
Db      960 GACATCTCTATCCACCCGAGCTCAAGAGGGCTCATGAAAGTGGAGAAATCGGCATGAA 1019

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QY      301 GlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLys 320
Db      1020 GGGCTCTCAAGTCTCTGGCTCCGAGGCTGGGCCCACTATGGGGCCAAAAGAAAAAG 1079

QY      321 AsnSerAsnMetThrTyrglnLysLeuSerArgAlaMetArgTyrrTyrrLysArgGlu 340
Db      1080 AACAGCAACATGACTCTTACAGAAAGCTGAGCCCGGCATAGGTACTTACAAACCGGAG 1139

QY      341 IleLeuGluArgValAspGlyArgArgLeuValTyrrLysPheGlyLysAsnSerSerGly 360
Db      1140 ATCTTGAAACGGGTGATGGCGGCACCTGCTTCAAACTTTGGCAAAACTCAAGCGGC 1199

QY      361 TrpLysGluGluGluValLeuGlnSerArgAsn 371
Db      1200 TGGAAAGAGAGAGAGGTTCTCCAGAGTCGGAAC 1232

RESULT 7
US-09-922-217-1105
; Sequence 1105, Application US/09922217
; Patent No. US2002007641A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Jiang, Yuguang
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922, 217
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-922-217-1105

Alignment Scores:
  pred. No.:      4,48e-219      Length:      1917
  Score:          1980.00         Matches:      371
  Percent Similarity: 100.00%     Conservative: 0
  Best Local Similarity: 100.00%   Mismatches:  0
  Query Match:    100.00%         Indels:      0
  DB:              9              Gaps:          0

US-08-978-217-2 (1-371) x US-09-922-217-1105 (1-1917)

QY      1 MetAlaAlaThrcysglulleserAnllepheserAntyrPheSerAlaMetTySer 20
Db      122 ATGGCTGCACCTGTGAGATTAGCAACATTTTAGCACTTCACTGAGTGAAGC 181

QY      21 SerGluAspSerThrleuAlaSerValProProAlaAlaThrPheGlyAlaAspAspLeu 40
Db      182 TCGGAGACTCCACCCCTGGCTCTGTTCCCTCTGCTCCACCTTTGGGGCCGATGACTTG 241

QY      41 ValLeuThrleuSerAspProGlnMetSerleuGluGlyThrGluValAspAspLeu 60
Db      242 GATCTGACCTTGAGCAACCCCAAGATGCTATGGAGGGTACAGAAAGGCGAGCTGGTGG 301

QY      61 GlyGluGlnProGlnPheTrpSerlyThrGlnValLeuAspTrpIleSerTyrglnVal 80
Db      302 GGGGAACAGCCCAAGTTCTGTGTAAGACCAAGTTCGATGATCACTGATCCAAAGTG 361

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QY 81 GtLysAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAspGlyAla 100
DB 362 GAGAAACAAGTACACCGCAAGCGCATTTGACTTCCAGAGTACATGATGGAGCGC 421
QY 101 ThrLeuCyAsnGlyAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 120
DB 422 ACCCTCTGCAATTGTCTCCCTTGAGGAGCTGCGTCTGGTCTTTGGGCTCTGGGGGACAA 481
QY 121 LeuHisAlaGluLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIle 140
DB 482 CTCACAGCCAGCTGGAGACCTCAGCTTCCAGCTTCTGATGAGCTCAGTTGATCATTT 541
QY 141 GluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
DB 542 GAGCTGCTGGAGAGATGGCATGGCTTCCAGAGGCCCTAGACCCAGGGCCCTTTGAC 601
QY 161 GlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis 180
DB 602 CAGGGAGGCCCTTTGCTCCAGAGAGCTGCTGAGACGAGCTCAGCAAGCCAGCCCTTACCAC 661
QY 181 ProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
DB 662 CCGGAGAGCTGTGGCCAGAGAGCCCTCCCTCCGAGAGCTTGAAGCTTCCAGCCAGAGG 721
QY 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp 220
DB 722 ACTGATGCTTCTCTGGAGCTCCAGCTCTCCAGATCCGGGTGAGAGTACGTGACCTGGAT 781
QY 221 ProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysLysGlyAspPro 240
DB 782 CCACATGATGGCAAGCTTTCCACAGAGATGTTTCTGTGATCTGCAAGAAAGGGGATCCC 841
QY 241 LysHisGlyLysArgLysArgLysArgProArgLysLeuSerLysGlyTyrTrpAspCys 260
DB 842 AAGCAGAGGAGAGGAGAAACAGAGCCGAGCCCGCAAACTGAGCAAAAGTACCTGGACTGT 901
QY 261 LeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArg 280
DB 902 CTCGAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 961
QY 281 AspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGln 300
DB 962 GACATCTCATCCACCAGGAGCTCAACGAGGGCTCATGAAAGTGGAGATCGCATGAA 1021
QY 301 GlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLys 320
DB 1022 GGGCTTTCAGAGTCTCCGCTCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1081
QY 321 AsnSerAsnMetThrTyrGlyLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGlu 340
DB 1082 AACAGCAACATGACCTTACGAGAGCTGAGCGGAGCCATGAGTACTTACAAACGAGAG 1141
QY 341 IleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSerGly 360
DB 1142 ATCTCTGGAACGGTGGATGGCCGCGCATCTGTTCAAGTTGGCAAAAACCTCAAGCGC 1201
QY 361 TrpLysGluGluGluValLeuGlnSerArgAsn 371
DB 1202 TGGAGAGAGAGAGAGTCTCCAGAGTCCGAGAC 1234

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; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skelley, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-1105

Alignment Scores:
Pred. No.: 4,48e-219 Length: 1917
Score: 1980.00 Matches: 371
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-08-978-217-2 (1-371) x US-10-025-380-1105 (1-1917)
QY 1 MetAlaAlaThrCysGluIleSerAsnIlePheSerAsnTyrPheSerAlaMetTyrSer 20
DB 122 ATGGCTGCAACCTGTGAGATTAGCAACATTTTATGCACTTCTCAGTGCATGATGAC 181
QY 21 SerGluAspSerThrLeuAlaSerValProAlaAlaThrPheGlyValAspAspLeu 40
DB 182 TGGAGAGATCCACCCCTGGCTCTGTCTCCCTGCTGACCACTTTGGGCGCATGCTTG 241
QY 41 ValLeuThrLeuSerAsnProGlnMetSerLeuGluGlyThrGluLysAlaSerTrpLeu 60
DB 242 GATCTGACCTTACAGCAACCCCGAGATGTCATTGAGAGGTACAGAGAGAGAGAGAGAG 301
QY 61 GlyGluGlnProGlnPheTrpSerLysThrGlnValLeuAspTrpIleSerTrpGlnVal 80
DB 302 GGGAGACAGCCCGAGTCTGTGTGAGAGACAGGTTCTGACTGATCAGTACCAAGTG 361
QY 81 GtLysAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAspGlyAla 100
DB 362 GAGAAACAAGTACACCGCAAGCGCATTTGACTTCCAGAGTACATGATGGAGCGC 421
QY 101 ThrLeuCyAsnGlyAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 120
DB 422 ACCCTCTGCAATTGTCTCCCTTGAGGAGCTGCGTCTGGTCTTTGGGCTCTGGGGGACAA 481
QY 121 LeuHisAlaGluLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIle 140
DB 482 CTCACAGCCAGCTGGAGACCTCAGCTTCCAGCTTCTGATGAGCTCAGTTGATCATTT 541
QY 141 GluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
DB 542 GAGCTGCTGGAGAGATGGCATGGCTTCCAGAGGCCCTAGACCCAGGGCCCTTTGAC 601
QY 161 GlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis 180
DB 602 CAGGGAGGCCCTTTGCTCCAGAGAGCTGCTGAGACGAGCTCAGCAAGCCAGCCCTTACCAC 661
QY 181 ProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
DB 662 CCGGAGAGCTGTGGCCAGAGAGCCCTCCCTCCGAGAGCTTGAAGCTTCCAGCCAGAGG 721
QY 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp 220

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 207
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-978-217-2
Alignment Scores:
Pred. No.: 4,74e-219 Length: 1996
Score: 1980.00 Matches: 371
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-08-978-217-2 (1-371) x US-09-925-301-207 (1-1996)
QY 1 MetAlaAlaThrCysGluIleSerAsnIlePheSerAsnIlePheSerAlaMetTyrSer 20
Db 141 ATGGCTGCAACCTGTGATGATTAACAATTATTTAGCAACTACTTCAAGTGGATGTACAGC 200
QY 21 SerGluAspSerThrLeuAlaSerValProProAlaAlaThrPheGlyAlaAspAspLeu 40
Db 201 TCGAGAGACTCCACCTCGGCTCTGTTCCTCCCTGCTGCCACTTTGGGGCGGATGACTTG 260
QY 41 ValLeuThrLeuSerAspProGlnMetSerLeuGluGlyThrGluValAsaSerTrpLeu 60
Db 261 GTACTGACCTTGAGCAACCCCGAGATGTCATTGAGGGTACAGAGAGGCCAGCTGGTTG 320
QY 61 GlyGluGlnProGlnPheTrpSerIleThrGlnValLeuAspTrpIleSerTyrGlnVal 80
Db 321 GGGGAAACGCCCCAGTTCTGTGGAAGACGCAAGTTCTGACAGGATCACTCAAGTG 380
QY 81 GluLysAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAspGlyAla 100
Db 381 GAGAAAGACAAAGTACGACGCAAGCGCCATTGACTTCCAGAGTGTACATGATGGGCC 440
QY 101 ThrLeuCysAsnCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 120
Db 441 ACCCTCTGCAATGTGCTTGAAGAGCTCGTGTGCTTGGGCTCTGGGGGACCA 500
QY 121 LeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIle 140
Db 501 CTCGATGCCAGCTGGAGAGACCTCACTCCAGCTCTTGTATGAGCTCAATTGGATCAT 560
QY 141 GluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
Db 561 GACCTGTGAGAGAGATGACATGGCTTCCAGAGGCCCTTACAGCCAGGCCCTTTGAC 620
QY 161 GluGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis 180
Db 621 CAGGGAGCCCCCTTTGCCAGAGACTGCTGAGACAGGTACAGAGCCACCTTACAC 680
QY 181 ProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
Db 681 CCGGGAGCTGTGGCGAGAGGCCCTCCCTCGGAGCTCTGACGCTCCACCGAGGG 740
QY 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyLysSerAspValAspLeuAsp 220
Db 741 ACTGGTCTCTCGAGACTCCCACTCTCAGACTCCCGGTGGAAGTGAAGTGGACCTGGAT 800
QY 221 ProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysGlyAspPro 240

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Db 801 CCACCTAGTGCAGAGCTTCCCAAGCATGTTTCGTGACTGCAAGAGGGGATCCC 860
QY 241 LysHisGlyLysArgLysArgGlyValArgProArgLysLeuSerLysGluTyrTrpAspCys 260
Db 861 AAGCAGGGAGACGGGAAAGAGAGCGCGCCCGAAGAGCTAGAGAAAGTACTGGGACTGT 920
QY 261 LeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArg 280
Db 921 CTCGAGGGCAAGAGAGCAAGACCGGCCCAAGAGGCCACCTGTGGAGTTCAATCCGG 980
QY 281 AspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGlu 300
Db 981 GACATCTCATCAACCGGAGCTCAACGAGGCGCTCATGAAGTGGAGAAATCGCATGAA 1040
QY 301 GlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTrpGlyLysLysLys 320
Db 1041 GGGCTCTCAAGTCTCTGGCTCCGAGGCTGGCCCACTATGGGGCCAAAAGAAAAG 1100
QY 321 AsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrTyrLysArgLys 340
Db 1101 AACAGCAATGACCTTACAGAGAGCTGAGCCGGCCATAGTACTACTACAAACGGAG 1160
QY 341 IleLeuGluArgValAspGlyValArgLeuValTyrLysPheGlyLysAsnSerSerGly 360
Db 1161 ATCTTGAAACGGGTGATGGCGGCGACTCGTCTACAACTTTGGCAAAAATCAAGCGGC 1220
QY 361 TrpLysGluGluGluValLeuGlnSerArgAsn 371
Db 1221 TGGAAAGAGAGAAAGAGTTCTCCAGAGTCCGAAC 1253

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RESULT 11

US-10-131-410-64

; Sequence 64, Application US/10131410

; Publication No. US20030235915A1

; GENERAL INFORMATION:

; APPLICANT: SPECHT, THOMAS

; APPLICANT: HINZMANN, BERND

; APPLICANT: SCHMITT, ARMIN

; APPLICANT: PILARSKI, CHRISTIAN

; APPLICANT: DAHL, EDGAR

; APPLICANT: ROSENTHAL, ANDRE

; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST

; FILE REFERENCE: SCH-1763

; CURRENT APPLICATION NUMBER: US/10/131,410

; PRIOR FILING DATE: 2002-04-25

; PRIOR APPLICATION NUMBER: 09/646,673

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: PCT/DE99/00908

; NUMBER OF SEQ ID NOS: 202

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 64

; LENGTH: 2269

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-131-410-64

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Alignment Scores:
Pred. No.: 3.6e-181 Length: 2269
Score: 1654.00 Matches: 315
Percent Similarity: 99.37% Conservative: 0
Best Local Similarity: 99.37% Mismatches: 2
Query Match: 83.54% Indels: 2
Gaps: 0
US-08-978-217-2 (1-371) x US-10-131-410-64 (1-2269)

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QY 55 GluLysAlaSerTrpLeuGlnGluGlnPheTrpSerLysThrGlnValLeuAsp 74
Db 15 GAGAAAGCAAGCTGTGGGGGAAAGAGCCCGGATCTGTGTCGAAGAG-CAGGTTCTGGAC 73

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; Sequence 853, Application US/09833263
; Patent No. US2002010547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833.263
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 853
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-833-263-853

Alignment Scores:
Pred. No.: 7.69e-121 Length: 626
Score: 1127.00 Matches: 208
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 56.92% Indels: 0
DB: 9 Gaps: 0

US-08-978-217-2 (1-371) x US-09-833-263-853 (1-626)

QY 53 G|YThrGluYsa|AsErTrPleuG|YgluG|nProG|nPhETpSerLyThrG|nVal 72
Db 624 GGTACAGAGAGGCGACCTGTTGGGGGAAACAGCCCGATTCGTGATGAGAGCGAGTT 565
QY 73 LeuAspTrpL|eSerTyRg|nValG|uLyAsnLyETrAsp|aSer|aIleaspPhe 92
Db 564 CTGGACCTGGATCGCTACCAAGTGGAGAAACAAAGTACGACGCGCATTTGACTTC 505
QY 93 SerArgCyAspMetAspG|yAlaThrLeuCyAsnCyAla|eug|uG|uLeuArgLeu 112
Db 504 TCACGATGTACATGATGATGGCGCCACCTCTGCATTTGCTCCCTTGGAGGCTGGCTG 445
QY 113 ValPheG|YPro|eug|YAspG|nLeuH|sAlaG|nLeuArgAspLeuThrSerSer 132
Db 444 GTCTTTGGGCTCTGGGGGACCACTCCATGCTGGAGACCTTCACTTCCAGCTCT 385
QY 133 SerAspG|uLeuSerTrpL|eIleG|uLeuLeuG|uLyAspG|yMetAlaPheG|nVal 152
Db 384 TCTGATGAGCTCACTTGGATCATTTGAGCTGCTGGAGAAAGATGGCATGGCTTCCAGAG 325
QY 153 AlaLeuAspProG|YProPheAspG|nG|ySerProPheAlaG|nValLeuLeuAsp 172
Db 324 GCCCTTACCCAGGCGCTTTGACCAAGGCGCCCTTTGCCAGAGCTGCTGGAGAC 265
QY 173 G|YGl|nG|nAlaSerProTyRHisProG|YSerCyeg|yAlaG|yAlaProSerProG|Y 192
Db 264 GGTAGAGAGCCAGCCCTTACCCAGGCGCTGTTGGAGAGAGAGAGAGAGAGAGAGAG 205
QY 193 SerSerAspValSerTrnAlaG|YThrG|YAlaSerArgSerSerHisSerSerAsp 212
Db 204 AGCTCTACGCTTCCACCGAGGAGCTGGCTTCTTGGAGCTTCCACTCTCCAGACTTC 145
QY 213 G|YGlYSerAspValaAspLeuAspProThraSpG|YLyLeuPheProSerAspG|YPhe 232
Db 144 GGTGGAAGTGCAGTGCAGCTGATGCCACTGATGGCAAGCTCTTCCCAAGAGTGT 85
QY 233 ArgSerCyAsnLySg|YAspProLyH|sG|YLySargLySargG|YArgProArgLyS 252
Db 84 CGTACTGCAAGAGGGGGATCCCAAGACGGAAGCGGAAGCGAGCCGCGCGGAAG 25
QY 253 LeuSerLySg|YTrPAspCyS 260
Db 24 CTGAGCAAGAGTACTGGAGCTGT 1
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RESULT 14
US-10-025-380-853/c
; Sequence 853, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Jiang, Yuguang
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 853
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-025-380-853

Alignment Scores:
Pred. No.: 7.69e-121 Length: 626
Score: 1127.00 Matches: 208
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 56.92% Indels: 0
DB: 13 Gaps: 0

US-08-978-217-2 (1-371) x US-10-025-380-853 (1-626)

QY 53 G|YThrGluYsa|AsErTrPleuG|YgluG|nProG|nPhETpSerLyThrG|nVal 72
Db 624 GGTACAGAGAGGCGACCTGTTGGGGGAAACAGCCCGATTCGTGATGAGAGCGAGTT 565
QY 73 LeuAspTrpL|eSerTyRg|nValG|uLyAsnLyETrAsp|aSer|aIleaspPhe 92
Db 564 CTGGACCTGGATCGCTACCAAGTGGAGAAACAAAGTACGACGCGCATTTGACTTC 505
QY 93 SerArgCyAspMetAspG|yAlaThrLeuCyAsnCyAla|eug|uG|uLeuArgLeu 112
Db 504 TCACGATGTACATGATGATGGCGCCACCTCTGCATTTGCTCCCTTGGAGGCTGGCTG 445
QY 113 ValPheG|YPro|eug|YAspG|nLeuH|sAlaG|nLeuArgAspLeuThrSerSer 132
Db 444 GTCTTTGGGCTCTGGGGGACCACTCCATGCTGGAGACCTTCACTTCCAGCTCT 385
QY 133 SerAspG|uLeuSerTrpL|eIleG|uLeuLeuG|uLyAspG|yMetAlaPheG|nVal 152
Db 384 TCTGATGAGCTCACTTGGATCATTTGAGCTGCTGGAGAAAGATGGCATGGCTTCCAGAG 325
QY 153 AlaLeuAspProG|YProPheAspG|nG|ySerProPheAlaG|nValLeuLeuAsp 172
Db 324 GCCCTTACCCAGGCGCTTTTGAACAGGCGCCCTTTGCCAGAGAGCTGCTGGAGAC 265
QY 173 G|YGl|nG|nAlaSerProTyRHisProG|YSerCyeg|yAlaG|yAlaProSerProG|Y 192
Db 264 GGTAGAGAGCCAGCCCTTACCCAGGCGCTGTTGGAGAGAGAGAGAGAGAGAGAGAG 205
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QY 193 SerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSer 212
Db 204 AGCTTACCTCTCCACCGAGGACTGTGCTTCTCGAGACTCCACTCTCCAGACTCC 145
QY 213 G1G1SerAspValAspLeuAspProThrAspGlyLeuPheProSerAspGlyPhe 232
Db 144 GGTGAAGTACCGGACCTGGATCCCATGATGGCAAGCTCTTCCCGCATGGTTT 85
QY 233 ArgAspCysHisGlyAspProLysHisGlyLysArgLysArgGlyArgProArgLys 252
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QY 253 LeuSerLysGlyLysTrpAspCys 260
Db 24 CTGAGCAAGAGTACTGGACTGT 1

RESULT 15
US-09-922-217-944/C
Sequence 944, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeline Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yugui
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 944
LENGTH: 563
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-217-944

Alignment Scores:
Pred. No.: 1,87e-107 Length: 563
Score: 1011.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.06% Indels: 0
Gaps: 0
DB: 9

US-08-978-217-2 (1-371) x US-09-922-217-944 (1-563)

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Db 562 GACTGGATCAGTACCAAGTGAAGAAACAAGTACGACCAAGCGCCATTGACTTCTCA 503
QY 94 ArgCysAspMetAspGlyAlaThrLeuCysAsnGlyAlaLeuGlnLysLeuArgLeuVal 113
Db 502 CGATGTGACATGATGGCGCCACTCTGCATTTGTCCCTTGAGGAGCTGCGTCTGTC 443
QY 114 PheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerSer 133
Db 442 TTGGGGCTTGGGGGACCACTCCATGCGCAGAGCTTCACCTTCAGCTTCT 383
QY 134 AspGlnLeuSerTrpIleIleGlnLeuLeuGlnLysAspGlyMetAlaPheGlnGlnAla 153
Db 382 GATGAGCTCAGTTGGATCATTTGAGCTGCTGGAAGAAGATGGCATGGCTTCCAGAGGCC 323
QY 154 LeuAspProGlyProPheAspGlnGlySerProPheAlaGlnGlnLeuLeuAspAspGly 173

Db 322 CTGACCCCAAGGCCCTTTGACCAAGGCAAGCCCTTTGGCCAGAGACTGTGACGACGAT 263
QY 174 GlnGlnAlaSerProTyrrHisPProGlySerCysGlyAlaGlyAlaAspSerProGlySer 193
Db 262 CACCAAGCCAGCCCTTACCAACCCCGGACACTGTGGCGCAAGAGCCCTTCCCGGCAAC 203
QY 194 SerAspValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGly 213
Db 202 TTGACGTCTCCACCGCAGGAGACTGTGCTTCTCGAGACTCCCATCTCTCAGACTCCGAT 143
QY 214 GlySerAspValAspLeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArg 233
Db 142 GGAAGTACGTGACCTGGATCCCACTGATGGCAAGCTCTTCCCGCATGATGGTTTCGT 83
QY 234 AspCysLysLysGlyAspProLysHisGlyLysArgLysArgGlyArgProArgLysLeu 253
Db 82 GACTGCAGAGAGGGGATCCCAAGCAGCGGAAGCGAAGCCGCGCCGGAAGCTG 23
QY 254 SerLysGlyLysTrpAspCys 260
Db 22 AGCAAGAGTACTGGACTGT 2

Search completed: November 16, 2004, 03:18:44
Job time : 648.855 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 14:00:59 ; Search time 114.561 Seconds
(without alignments)
2301.862 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues
Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued Patents NA -QPMT=fastap -SUPPFX=tni -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdt
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
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5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1980	100.0	1907	4	US-09-300-958A-27
2	1980	100.0	1907	4	US-09-570-593-4
3	1980	100.0	1920	1	US-08-746-789A-1
4	903	45.6	502	4	US-09-389-681-282
5	903	45.6	502	4	US-09-620-405B-282
6	903	45.6	502	4	US-09-339-338-282
7	903	45.6	502	4	US-09-433-826B-282
8	903	45.6	502	4	US-09-604-287A-282
9	903	45.6	502	4	US-09-834-759-282
10	903	45.6	502	4	US-09-590-751A-282
11	559	28.2	5427	3	US-09-009-913-2
12	555.5	28.1	5510	3	US-09-009-913-3

13	555.5	28.1	5667	3	US-09-009-913-4	Sequence 4, Appl1
14	519.5	26.2	852	3	US-09-020-956-44	Sequence 44, Appl1
15	519.5	26.2	852	3	US-09-030-607-44	Sequence 44, Appl1
16	519.5	26.2	852	3	US-09-439-313-44	Sequence 44, Appl1
17	519.5	26.2	852	3	US-09-352-616A-44	Sequence 44, Appl1
18	519.5	26.2	852	4	US-09-232-149A-44	Sequence 44, Appl1
19	519.5	26.2	852	4	US-09-159-812-44	Sequence 44, Appl1
20	519.5	26.2	852	4	US-09-636-215-44	Sequence 44, Appl1
21	519.5	26.2	852	4	US-09-685-166A-44	Sequence 44, Appl1
22	519.5	26.2	852	4	US-09-115-453-44	Sequence 44, Appl1
23	519.5	26.2	852	4	US-09-688-489-44	Sequence 44, Appl1
24	519.5	26.2	852	4	US-09-679-426-44	Sequence 44, Appl1
25	486.5	24.6	848	3	US-09-009-913-338	Sequence 338, App
26	432	21.3	2280	3	US-09-009-913-6	Sequence 6, Appl1
27	432	21.3	2428	3	US-09-009-913-6	Sequence 6, Appl1
28	432	21.3	2498	3	US-09-009-913-10	Sequence 10, Appl1
29	281	14.2	237	4	US-09-016-434-927	Sequence 927, App
30	246.5	12.4	2375	1	US-08-368-281-1	Sequence 1, Appl1
31	242	12.2	3340	1	US-08-368-281-3	Sequence 1, Appl1
32	238.5	12.0	1894	4	US-09-570-593-1	Sequence 1, Appl1
33	238.5	12.0	1905	3	US-09-055-113-2	Sequence 2, Appl1
34	238.5	12.0	3317	4	US-09-570-593-12	Sequence 12, Appl1
35	234.5	11.8	1752	3	US-09-360-779-1	Sequence 1, Appl1
36	234.5	11.8	1752	3	US-09-435-335-1	Sequence 1, Appl1
37	233	11.8	2268	3	US-09-344-579-1	Sequence 1, Appl1
38	228	11.5	1604	5	US-08-306-691B-43	Sequence 43, Appl1
39	228	11.5	1604	5	PCT-US93-06251-9	Sequence 9, Appl1
40	214.5	10.8	1933	4	US-09-920-759-3	Sequence 3, Appl1
41	214.5	10.8	1936	4	US-09-920-759-10	Sequence 10, Appl1
42	213.5	10.8	1528	4	US-08-878-177-3	Sequence 3, Appl1
43	212	10.7	2938	2	US-08-343-443B-3	Sequence 1, Appl1
44	207	10.5	1447	3	US-08-878-177-1	Sequence 1, Appl1
45	205.5	10.4	454	4	US-09-270-767-10903	Sequence 10903, A

ALIGNMENTS

RESULT 1
US-09-300-958A-27
Sequence 27, Application US/09300958A
Patent No. 6495319
GENERAL INFORMATION:
APPLICANT: McCrelland, Michael
APPLICANT: Welch, John
APPLICANT: Trenkle, Thomas
TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
FILE REFERENCE: P-PH 3457
CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/098,070
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/116,624
PRIOR FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 1907
TYPE: DNA
ORGANISM: Homo sapiens
US-09-300-958A-27
Alignment Scores:
Pred. No.: 2.49e-191
Score: 1980.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0
Length: 1907
Matches: 371
Conservative: 0
Mismatch: 0
Indels: 0

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 Db ATGGCTCAACCTGTGAGATTAGCAACATTTTGTAGCAACTACTTCAGTGGCATGTACAGC 155
 QY 21 SerGluAspSerThrLeuAlaSerValProProAlaIaIaThrPheGlyAlaAspAspLeu 40
 Db TCGGAGAGACTCCACCTGGCTCTGTGTCCCTGTCTCCACCTTTGGGGCCGAGACTTG 215
 QY 41 ValLeuThrLeuSerAspProGluMetSerLeuGluGlyThrGluValAspTyrLeu 60
 Db GTACTGACCTTGAGCAACCCCGAGATGTACTTGAAGGTACAGAGAGCCAGCTGGTTG 215
 QY 61 GlyGluGlnProGlnPheTyrPheTyrSerGluValLeuAspTyrIleSerTyrGlnVal 80
 Db GGGGAAACAGCCCGAGTCTGGTCAAGACGAGGTTCTGGAGCTGATCACTACCAAGTG 335
 QY 81 GluIleAsnIleTyrAspAlaSerAlaIleAspPheSerTyrGlyAspMetAspGlyAla 100
 Db GAGAAAGAACAGTACGAGCAGGCGCATTCACAGATGTACATGATGATGGCGCC 395
 QY 101 ThrLeuCysAsnCybAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGln 120
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 QY 121 LeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTyrIleIle 140
 Db CTCATGCTCCAGCTGCGAGACCTCACTTCAGCTCTTCTGATGAGCTCAGTTGGATCAT 515
 QY 141 GluLeuLeuGluIleAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
 Db GAGCTGTGAGAGAGATGATGCTCTTCAGAGAGCCCTTACAGCCAGGCCCTTTGAC 575
 QY 161 GlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis 180
 Db CAGGGCAGCCCTTTGCTGCGAGAGCTCTGACAGACGTCAGCAAGCCACCTTACAC 635
 QY 181 ProGlySerCysGlyAlaGlyAlaAspSerProGlySerSerAspValSerThrAlaGly 200
 Db CCCGGCAGCTGTGGCGCAGAGAGCCCTCCCTGGCAGCTCTGACGCTCCACGCGAGGG 695
 QY 201 ThrGlyAlaSerTyrSerSerHisSerSerAspSerTyrGlySerAspValAspLeuAsp 220
 Db ACTGGTCTCTCGAGACTCCCACTCTCAGACTCCGCTGAGAGTACGAGTGGACTGGAT 755
 QY 221 ProThrAspGlyIleLeuPheProSerAspGlyPheArgAspCysIleValAspPro 240
 Db CCACATGATGGCAAGCTCTTCCCGAGGATGTTTCTGATGCTGCAAGAGAGGGGATCCC 815
 QY 241 LysHisGlyIleValArgIleValArgProArgIleValSerIleValTyrTyrAspCys 260
 Db AAGCAGCGGAGAGCGAAGACAGGCGCGGCCCGAAGAGTGAAGAGTCTGGGACTGT 875
 QY 261 LeuGluGlnIleValSerIleValAlaProArgGlyThrHisIleuTyrPheGluPheIleArg 280
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 QY 301 GlyValPheIleValSerIleValAlaValAlaGlnLeuTyrPheGlyIleValVal 320
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QY 361 TrrPheGluGluGluValLeuGlnSerArgAsn 371
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 RESULT 2
 US-09-570-593-4
 ; Sequence 4, Application US/09570593
 ; Patent No. 6566063
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaufmann, Joerg
 ; APPLICANT: Xin, Hong
 ; APPLICANT: Hartowe, Greg
 ; TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
 ; FILE OF INVENTION: CANCER
 ; FILE REFERENCE: 2300-1556
 ; CURRENT APPLICATION NUMBER: US/09/570,593
 ; PRIOR FILING DATE: 2000-05-12
 ; PRIOR APPLICATION NUMBER: 60/134,112
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (96)...(1211)
 ; OTHER INFORMATION: Human epithelial-restricted with serine box (BSX)
 ; OTHER INFORMATION: protein.
 US-09-570-593-4
 Alignment Scores:
 Pred. No.: 2,496-191 Length: 1907
 Score: 1980.00 Matches: 371
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-08-978-217-2 (1-371) x US-09-570-593-4 (1-1907)
 QY 1 MetAlaIaThrCysGluIleSerAsnIlePheSerAntyrPheSerAlaMetTyrSer 20
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 QY 21 SerGluAspSerThrLeuAlaSerValProProAlaIaIaThrPheGlyAlaAspAspLeu 40
 Db TCGGAGAGACTCCACCTGGCTCTGTGTCCCTGTCTCCACCTTTGGGGCCGAGACTTG 215
 QY 41 ValLeuThrLeuSerAspProGluMetSerLeuGluGlyThrGluValAspTyrLeu 60
 Db GTACTGACCTTGAGCAACCCCGAGATGTACTTGAAGGTACAGAGAGCCAGCTGGTTG 275
 QY 61 GlyGluGlnProGlnPheTyrPheTyrSerGluValLeuAspTyrIleSerTyrGlnVal 80
 Db GGGGAAACAGCCCGAGTCTGGTCAAGACGAGGTTCTGGAGCTGATCACTACCAAGTG 335
 QY 81 GluIleAsnIleTyrAspAlaSerAlaIleAspPheSerTyrGlyAspMetAspGlyAla 100
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 QY 121 LeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGluLeuSerTyrIleIle 140
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 QY 141 GluLeuLeuGluIleAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160
 Db GAGCTGTGAGAGAGATGATGCTCTTCAGAGAGCCCTTACAGCCAGGCCCTTTGAC 575

QY 161 GlnGlySerProPheAlaGlnGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis 180
 DB 576 CAGGAGACCCCTTTTCCCGAGAGCTGCTGAGACGCTGACGAGACGAGCCCTTACAC 635
 QY 181 ProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspAlaSerThrAlaGly 200
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 QY 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp 220
 DB 696 ACTGTCCTTCTCTGAGAGCTCCCACTCTCACTCGGTGAGAGTACAGTGAGCTGAGAT 755
 QY 221 ProThrAspGlyAlaSerLeuPheProSerAspGlyPheAspAspCysIleValSerGlyAspPro 240
 DB 756 CCACGTGATGGCAAGCTCTTCCCGAGAGATGTTTCTGATCTGACAGAGAGAGGAGATCCC 815
 QY 241 LysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTyrTyrAspCys 260
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 DB 1176 TGGAGAGAGAGAAAGATTCTCCAGAGTCGAGAC 1208
 RESULT 3
 US-08-746-789A-1
 ; Sequence 1, Application US/08746789A
 ; Patent No. 5789200
 ; GENERAL INFORMATION:
 ; APPLICANT: Ismail Kola, Martin J. Tyms, Christine DeBuck
 ; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ERF3
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road, P.O. Box 1539
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM 486
 ; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
 ; SOFTWARE: MICROSOFT WORD
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/746,789A
 ; FILING DATE: No. 5789200ember 15, 1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:

; NAME: William T. Han
 ; REGISTRATION NUMBER: 34,344
 ; REFERENCE/DOCKET NUMBER: ATG 50024
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610 270 5219
 ; TELEFAX: 610 270 4026
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1920
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; ANTI-SENSE: NO
 ; US-08-746-789A-1
 Alignment Scores:
 Pred. No.: 2,52e-191 Length: 1920
 Score: 1980.00 Matches: 371
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0
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 DB 115 ATGGCTGCACTGTGAGATTGACACATTTTATGCACTTCTCAGTCGATGACAC 174
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 DB 175 TGGAGAGATCTCAACCTGGCTGTGTTCCCTGCTGCGACCTTGGGGCCGATGACTTG 234
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 DB 235 GACTGACCCCTGAGCAACCCCGAGATGTCATGAGAGGTACAGAGAGCTGAGTGG 294
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 DB 295 GGGGAAACAGCCAGTTCGTGTGAGAGAGCGAGTTCTGACTGATCAGTACCAAGTG 354
 QY 81 GlyLysAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAspGlyAla 100
 DB 355 GAGAAAGAAAGTACAGACCAAGCGCATTTGACTTCCAGATGATGATGGAGGCC 414
 QY 101 ThrLeuCysAsnCysAlaLeuGlnGlnLeuValPheGlyProLeuGlyAspGln 120
 DB 415 ACCCTGCAATTGTGCCCTTGAGAGAGCTGCTGTGCTTGGGGCTTGGGGGAGACAA 474
 QY 121 LeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGlnLeuSerTyrIleIle 140
 DB 475 CTCACAGCCAGCTGGAGAACCTCACTTCACCTCTTCTGATGAGCTCAGTTGATCAAT 534
 QY 141 GluLeuLeuGlnLysAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyProPheAsp 160
 DB 535 GAGCTCTGAGAAAGATGGCATGGCTTCCAGAGAGCCCTTGAACCAAGGCCCTTTGAC 594
 QY 161 GlnGlySerProPheAlaGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerProTyrHis 180
 DB 595 CAGGAGAGCCCTTTTCCCGAGAGCTGAGAGAGCTGAGAGCTGAGAGAGCCCTTACAC 654
 QY 181 ProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200
 DB 655 CCGGAGAGCTGTGCGCAGAGAGCCCTTCCCTGAGAGCTGTGACCTTCCACCGAGAG 714
 QY 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAsp 220
 DB 715 ACTGTCCTTCTCTGAGAGCTCCCACTCTCACTCGGTGAGAGTACAGTCACTGAGAT 774
 QY 221 ProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysIleValSerGlyAspPro 240
 DB 775 CCACGTGATGGCAAGCTTCCCGAGAGATGTTTCTGATCTGACAGAGAGAGGAGATCCC 834

Qy		241	LvSHIGlYlvbArgrglvArgrglvAProARgLvlsEulerlyeGlUtyTrPAsrCyS	260
Db		835	AAGCAGGGGAAAGCGAAACGAAGCCGCCGCCGAAAGCTTAGCAAAAGATGTGGGACTGT	894
Qy		261	LeuGIUGlYlvbArgrSerlySHIsAlAProARgLTThShISleuITrdJluARHeIleArq	280
Db		895	CTCGAGGCGCAGAGNAGCANGCACGGCCCCAGAGGACCACCTGTGGAGTTCAATCCGG	954
Qy		281	ASpIleuIlshIsAProgluleuAnenglUglyeMeLyseITrdJluANArghISglu	300
Db		955	GACATCTCATTCACCCCGGAGCTCAACGAGGGGCTCATGAAGTGGAGAAATCGCATGMA	1011
Qy		301	GIvAlPhelylePheleuArgrSerGUAlAvAlAlAgInleuITrdJlUlnlyslvlys	320
Db		1015	GGGGCTTCAAGATTCTCGGCTCCGAGGCTGrRGCCCACTATGGGGCGCAAAAAG	1074
Qy		321	AnrSerAsmecthLyrgrglvylvsEulerArGLAMetArITyTrTyTrlySArgrlu	340
Db		1075	AACAGCAACATGACCTTAACGAAAGCTGAGCGGGCCATAGGTACTACTACNAACGGAG	1133
Qy		341	IleLeuglunArgrValaspglvArgrgleuValTyTrlySPheglYlvshAnserserjly	360
Db		1135	ATCTCGAAGCGGTGATGGCCGGCAGACTGTCTACAATTGGCAAAACCTCAAGCGGC	1199
Qy		361	TtPlYegLUglUglUnVAlleugInserArghAn	371
Db		1195	TGGNAGGAGAGAGAGGTTCTCCAGACTCGGAAC	1227
RESULT 4				
US-09-389-681-282	/ Sequence 282, Application US/09389681A			
/ Patent No. 6518237				
/ GENERAL INFORMATION:				
/ APPLICANT: Yugui, Jiang				
/ APPLICANT: Dillon, David C.				
/ APPLICANT: Mitcham, Jennifer L.				
/ APPLICANT: Xu, Jiaochun				
/ TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND				
/ FILE REFERENCE: 210121.470C3				
/ CURRENT APPLICATION NUMBER: US/09/389,681A				
/ CURRENT FILING DATE: 1999-09-02				
/ NUMBER OF SEQ ID NOS: 463				
/ SOFTWARE: FastSeq for Windows Version 3.0				
/ SEQ ID NO 282				
/ LENGTH: 502				
/ TYPE: DNA				
/ ORGANISM: Homo sapiens				
US-09-389-681-282				
Alignment Scores:				
Pred. No.:	8,97e-83	Length:	502	
Score:	903.00	Matches:	166	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	45.61%	Indels:	0	
DB:	4	Gaps:	0	
US-08-978-217-2 (1-371) x US-09-389-681-282 (1-502)				
Qy		184	CyegIvAlaGlYvAlAProSerPrOglYSerSerASPvAlSeThAlAgIlyThrGlYAla	203
Db		3	TGTGGCGCAGAGAACCCCCTCCCGGCAAGCTTGACGTCTCCACCGCAGAGACTGTGCT	62
Db		204	SetArSerSerISerISerSerArppSerGlyGlySerASPvAlAspleuAspProthrArp	223
Db		63	TCTCGAGAGCTCCACACTCTTCAGACTCCGGGGAAGGAGGTGACCTTGATCCCACTGAT	122
Qy		224	GIvLYleuPheProSerArpgIYPheArgrAspCYvlyeLyglYvAspProlySHIsagIy	243
Db		123	GGCAGAGCTTCTCCCGCACGATGTATTTTCGTGACTGCAGAAAGGGGATCCCAAGCACGG	182
Qy		244	LvARglvArgrglvArgrProARgLvlsEulerlyeGlUtyTrPAsrCySleuGlUgly	263

Db	183	AAAGCGAAACGAGGCGCGCCGCGAAAGCTGACGAAAGATGCTGGAGCTGCTCGAAGGC	242
Qy	264	LYELYSERLYEHIALAProAgtgLYThrhIsleuTPGluPheIIeaArgpIleu	263
Db	243	AAAGAAAGCAAGCAGCGCCGACAGAGCAACCCACTGTGGAGTTTCATCCGGGACATCTC	302
Qy	284	IIeHAPRoGluLeuAmsnIuIlyeUmetLystrPGIuaaAaRghIaGIuGLyValPhe	303
Db	303	ATCACCCGGAAGCTCAACAGAGGCGCTCATGAAGTGGAGAAATCGGCAATGAAGGCGTCTTC	362
Qy	304	LYEPheLeuArgSerSILuaIaValaIaGluLeuTPGlyGlnLYsLYsAAsnSerAsn	333
Db	363	AAAGTCTGTGGCTCCAGAGCTGTGGCCCACTATGGGCCCAAAAAGAAAAGAACAGCAAC	422
Qy	324	MeethrLYGluLYsLeuSerAArgaIaAeAArgLYTYTYLYsAArgGluIleLeuGlu	343
Db	423	ATGACCTACAGAAAGCTGAGCGGGCCATAGAGTACTACTCAAAACGGAGATCTCGAA	482
Qy	344	ArgValAspGLyArgArg 349	
Db	483	CGGAGTGAATGGCCGCGCA 500	
RESULT 5			
US-09-620-405B-282			
; Sequence 282, Application US/09620405B			
; Patent No. 6528054			
; GENERAL INFORMATION:			
; APPLICANT: Jiang, Yugu			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Harlocker, Susan L.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; FILE REFERENCE: 210121.470C8			
; CURRENT APPLICATION NUMBER: US/09/620.405B			
; CURRENT FILING DATE: 2000-07-20			
; NUMBER OF SEQ ID NOS: 495			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 282			
; LENGTH: 502			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-620-405B-282			
Alignment Scores:			
Pred. NO.: 8.97e-83			
Score: 903.00			
Best Local Similarity: 100.00%			
Query Match: 45.61%			
DB: 4			
US-08-978-217-2 (1-371) x US-09-620-405B-282 (1-502)			
Qy	184	CyGGLYALaGLyLaProSerProGlySerSerAAspValSerThrAlaGLYThrhLYaLa	203
Db	3	TGTGGCCCAAGACCCCTCTCCCGGCAAGCTTGACGTCTCCACGCGCAGGAGCTGTGCT	62
Qy	204	SeArGerSerIIsSerSerAAspSerGlyGlySerAAspValAAspLeuAAspProThrAAsp	223
Db	63	TCTCGAGCTCCCACTCTCAAGCTCGGTGAAATGAATGACGTGGATCCCACTGAT	122
Qy	224	GLYLYsLeuPheProSerAAspGLyPheArgAAspCYsLYsLYsGLyAAspProLYsHISGLY	243
Db	123	GGCAAGCTTCTCCCAAGCATGTGTTTGTGTACTCAAGAAAGGGGAGATCCCAAGCAGGG	182
Qy	244	LYeAArgLYsArgGLyArgProArgArgLYsLeuSerLYsLYsLYsLYsLYsLYsLYsLYs	265
Db	183	AAAGGAAAGAGAGCGGCGCCGAAAGCTGACAAAGATGACTGGAGTGTCTTGAGGGC	242

QY 264 LysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeu 283
 DB 243 AAGAAGAGCAAGACCGCCGACAGAGCACCACTGTGGAGATTTCATCCGGGACATCTTC 302
 QY 284 ILeHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGluValPhe 303
 DB 303 ATCCACCCCGAGACTCAACAGAGGCTCCATGAGTGGAGAAATCGGATGAAGCGCTTTC 362
 QY 304 LysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGluLysLysAsnSerAsn 323
 DB 363 AAGTTCCTCCGCTCCAGAGCTGTGGCCCACTATGGGGCCAAAGAAAGAAAGACAGCAAC 422
 QY 324 MetThrTyrgLysLysLeuSerArgAlaMetArgTyrrTyrrLysArgGluIleLeuGlu 343
 DB 423 ATGACCTACGAGAGAGTGAAGCGGCGCATGAGGTACTACTACAAACGGGAGATCTCGAA 482
 QY 344 ArgValAspGlyArgArg 349
 DB 483 CGGATGATGCGCGGCGA 500

RESULT 6

US-09-339-338-282
 ; Sequence 282, Application US/09339338A
 ; Patent No. 6573368
 ; GENERAL INFORMATION:
 ; APPLICANT: Yugui, Jiang
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiangchun
 ; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.470C2
 ; CURRENT APPLICATION NUMBER: US/09/339,338A
 ; NUMBER OF SEQ ID NOS: 315
 ; SOFTWARE: FASTSEQ for windows Version 3.0
 ; SEQ ID NO 282
 ; LENGTH: 502
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-339-338-282

Alignment Scores:

Pred. No.: 8,97e-83 Length: 502
 Score: 903.00 Matches: 166
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 45.61% Indels: 0
 DB: 4 Gaps: 0

US-08-978-217-2 (1-371) x US-09-339-338-282 (1-502)

QY 184 CysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAla 203
 DB 3 TGTGGCGAGAGAGCCCTCCCTCCCGAGCTGTGAGCTCCACCGCAGGAGACTGTGTCT 62
 QY 204 SerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAsp 223
 DB 63 TCTCGAGCTCCACACTCTCAGACTCCGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 122
 QY 224 GlyLysLeuPheProSerAspGlyPheArgAspCysLysGlyAspProLysHisGly 243
 DB 123 GCGAAGCTCTTCCCGCAGCGATGGTTCGTCGACTGCAAGAGGGGATCCCAAGCAGCGG 182
 QY 244 LysArgLysArgGlyArgProArgLysLysSerLysGlyLysTrpAspCysLeuGluGly 263
 DB 183 AAGCGAAGAGAGAGCGCGCCGAAAGCTGAGCAAGAGTACTGGGACTGTCTCGAGGGC 242
 QY 264 LysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeu 283
 DB 243 AAGAAGAGCAAGACCGCCGACAGAGCACCACTGTGGAGATTTCATCCGGGACATCTTC 302
 QY 284 ILeHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGluValPhe 303

DB 303 ATCCACCCCGAGACTCAACAGAGGCTCCATGAAGTGGAGAAATCGGATGAAGCGCTTTC 362
 QY 304 LysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGluLysLysAsnSerAsn 323
 DB 363 AAGTTCCTCCGCTCCAGAGCTGTGGCCCACTATGGGGCCAAAGAAAGAAAGACAGCAAC 422
 QY 324 MetThrTyrgLysLysLeuSerArgAlaMetArgTyrrTyrrLysArgGluIleLeuGlu 343
 DB 423 ATGACCTACGAGAGAGTGAAGCGGCGCATGAGGTACTACTACAAACGGGAGATCTCGAA 482
 QY 344 ArgValAspGlyArgArg 349
 DB 483 CGGATGATGCGCGGCGA 500

RESULT 7

US-09-433-826B-282
 ; Sequence 282, Application US/09433826B
 ; Patent No. 6579973
 ; GENERAL INFORMATION:
 ; APPLICANT: Yugui, Jiang
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Harkocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.470C4
 ; CURRENT APPLICATION NUMBER: US/09/433,826B
 ; NUMBER OF SEQ ID NOS: 474
 ; SOFTWARE: FASTSEQ for windows Version 3.0
 ; SEQ ID NO 282
 ; LENGTH: 502
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-433-826B-282

Alignment Scores:

Pred. No.: 8,97e-83 Length: 502
 Score: 903.00 Matches: 166
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 45.61% Indels: 0
 DB: 4 Gaps: 0

US-08-978-217-2 (1-371) x US-09-433-826B-282 (1-502)

QY 184 CysGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAla 203
 DB 3 TGTGGCGAGAGAGCCCTCCCTCCCGAGCTGTGAGCTCCACCGCAGGAGACTGTGTCT 62
 QY 204 SerArgSerSerHisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAsp 223
 DB 63 TCTCGAGCTCCACACTCTCAGACTCCGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 122
 QY 224 GlyLysLeuPheProSerAspGlyPheArgAspCysLysGlyAspProLysHisGly 243
 DB 123 GCGAAGCTCTTCCCGCAGCGATGGTTCGTCGACTGCAAGAGGGGATCCCAAGCAGCGG 182
 QY 244 LysArgLysArgGlyArgProArgLysLysSerLysGlyLysTrpAspCysLeuGluGly 263
 DB 183 AAGCGAAGAGAGAGCGCGCCGAAAGCTGAGCAAGAGTACTGGGACTGTCTCGAGGGC 242
 QY 264 LysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeu 283
 DB 243 AAGAAGAGCAAGACCGCCGACAGAGCACCACTGTGGAGATTTCATCCGGGACATCTTC 302
 QY 284 ILeHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGluValPhe 303
 DB 303 ATCCACCCCGAGACTCAACAGAGGCTCCATGAGTGGAGAAATCGGATGAAGCGCTTTC 362
 QY 304 LysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGluLysLysAsnSerAsn 323

[illegible]

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Db          483 CGGGTGTATGCCGCGCA 500

RESULT 11
US-09-009-913-2
; Sequence 2, Application US/0900913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axy's Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5427 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
;
US-09-009-913-2

Alignment Scores:
Pred. No.:      2.98e-46      Length:      5427
Score:          559.00       Matches:     140
Percent Similarity: 47.42%   Conservatve: 44
Best Local Similarity: 36.08% Mismatches:    88
Query Match:      28.23%     Indels:      116
DB:                3        Gaps:         12

US-08-978-217-2 (1-371) x US-09-009-913-2 (1-5427)

QY      27 AlaseValProPrOlaIaThr-----PegLIyAlaaspPLeuValleuThr 43
      ||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db      84 GCTCCCTCCCCTCATCAGCACACAGTAGTGATTTCACACCAGAATCTTTAGTA--- 140
      |||||
QY      44 LeusenRanDroginMetSerIeuInguLy----- 53
      ||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db      141 -----AATGATGCATGATTCTGGAAAGAGGTGTGAATGAATCTAACCCCGCAAC 194
      |||||
QY      54 -----ThrgIuYsaIaseP----- 58
      |||||
Db      195 AACCTCCTTACCAAGCCGCCAGCTGGACAGACACTACTCCACGTGCATGTTTCCAGT 255
      |||||
QY      59 -----TrpleuGIyuInProgiNphetipSerLyethrGIuVal 72
      |||||
Db      255 GGGTTTTTTGGAGCCAGTGCATGAATAATTCACTCTCAAGTACTGACCAAGTTACCAAGT 314
      |||||
QY      73 LeuapTrIpIleSerTyrgInValGIuYsaenLyTYraSpAlaseValIeIsPhe 92

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Db      315 TGGAGAGGCTCCAGCACTCTCGAGACCAACACGATGACAAATTGATCCCTTTC
Qy      93 SerArgCysAspMetAspGlyAlaThrLeuCysAspGlyAlaLeuGluGluLeuArgLeu
Db      375 CAAGAGTTCACATCAACGGCGAGCACCTCTCGAGCATGAGTTTGACGGAGTTCAACCCGG
Qy      113 ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr-----
Db      435 GCGGACGAGACGGCGGGGAGCTCTCTACAGCAAACTTGACGATCTGAAGTGGACGGC
Qy      130 SerSerSerSerSerAspGluLeuSerTrpIleIleGluLeuLeuGluValAspGlyMetAla
Db      495 CAGTCGAGTAGTGAC-----CTG
Qy      150 PheGlnIleuAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGlnGluLeu
Db      513 TTCACATGCC-----ACACACAAATGTC
Qy      170 LeuAspAspGlyGlnGlnAlaSerProTyrlHisProGlySerCysGlyAlaGlyAlaPro
Db      534 ATGTGCAAGACTGAACAAACTGAGCCT-----
Qy      190 SerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSer
Db      561 -----TCCATCATGAACACCTGGAAGACGAACTATTATAT
Qy      210 SerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyValLeuPheProSer
Db      600 GACACCACTATGTTGACACAGTATGTTG-----TTGACAGCAAAACTTTC-----
Qy      230 AspGlyPheArgAspCysValys-----
Db      648 -----TCCGCGGCTCAGATCTCCATGACCAACACACGATCCTTCTGTT
Qy      238 GlyAspProLysHisGlyValArgValArgGlyAlaArgProArgLysLeuSerLysGluTyr
Db      693 GCAGAGTCACCTGATATGAAAGAGCAAGACCCCTCCAAAGTCCACACCAAA---
Qy      258 TrpAspCysLeuGluGlyLysSerLysHisAlaProArgGlyThrHisLeuTrpGlu
Db      750 -----AACCAACAACCCGAGAGGACTCCTTATGGAA
Qy      278 PheIleArgAspIleLeuIleHisProGluLeuAsnGluLysLeuMetLysTrpGluAsn
Db      783 TTCATCCGACATCTCTTGAACCCAGACAAAGAACCCAGATTATTAATGGAAGAC
Qy      298 ArgHisGlnGlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTrpGlyGln
Db      843 CGATCTGAGGGCGCTTCAGGTTCTTGAAATCAGAGGACGTGCTCAGCTATGGGTAAA
Qy      318 LysLysLysAspSerAspMetTrpGlyLysLeuSerArgAlaMetArgTyrTyrTyr
Db      903 AAGAAAGAAACAACGACGACATGAAAGCTGACCGAGCTATGAAATTTACTAC
Qy      338 LysArgGlnIleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsn
Db      963 AAAAAGAAATACTGAGCGCTGTGATGAGCAAGAACTGATATATAATTGGGAAGAAAT
Qy      358 SerSerGlyTrpLysGlnGlu 365
Db      1023 GCCCGAGATGAGAGAAATGAA 1046

```

RESULT 12

US-09-009-913-3

Sequence 3, Application US/0909913

Patent No. 6087485

GENERAL INFORMATION:

APPLICANT: Axy's Pharmaceuticals, Inc.

TITLE OF INVENTION: Asthma Related Genes

NUMBER OF SEQUENCES: 339

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bozicevic & Reed, LLP

```

/ STREET: 285 Hamilton Ave, Suite 200
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ FILING DATE: 21-JAN-1998
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sherwood, Pamela J
/ REGISTRATION NUMBER: 36,677
/ REFERENCE/DOCKET NUMBER: SEQ-4P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-327-3231
/ TELEFAX: 650-327-3231
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5510 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-09-009-913-3

Alignment Scores:
Pred. No.: 6,92e-46 Length: 5510
Score: 555.50 Matches: 126
Percent Similarity: 51.24% Conservative: 39
Best Local Similarity: 39.13% Mismatches: 78
Query Match: 26.06% Indels: 79
DB: Gaps: 8

US-08-978-217-2 (1-371) x US-09-009-913-3 (1-5510)
Qy      59 TrpLeuGlyGluGlnProGlnPheTrpSerLysThrGlnValLeuAspTrpIleSerTyr
Db      356 TGGCATGAATTCATCTCTGATGACTGACCAAGTACAGAGTGTGGAGTGGCTCCAGCAC
Qy      79 GlnValGlnLysAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAsp
Db      416 CTCCTGACACCAACGACGCTGATGCAATTGTATCCCTTCCAAAGATTGACATCAAC
Qy      99 GlyAlaThrLeuCysAspAsnGlyAlaLeuGluGluValPheGlyProLeuGly
Db      476 GGGGACACCTCTGCGACATGAGTTTGACAGAGTTCAACCGGGGCGGAGACGGCGGG
Qy      119 AspGlnLeuHisAlaGlnLeuArgAspLeuThr-----SerSerSerSerAspGlu
Db      536 CAGCTCTCTACAGCAAACTTGACGATCTGAAGTGAAGGCGCAAGTCAGTATGAC---
Qy      136 LeuSerTrpIleIleGluLeuLeuGluValAspGlyMetAlaPheGlnGlnAlaLeuAsp
Db      593 -----CTGTTCACATGCC-----
Qy      156 ProGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGln
Db      605 -----ACACACAAATGCTCAAGACTGAACAA
Qy      176 AlaSerProTyrlHisProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAsp
Db      635 ACTGAGCCT-----
Qy      196 ValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyLys

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Db      644 ---TCATCATGAACCTGTAAGAGAGAGAACTATTATATGACCAACATATGGTAGC 700
Qy      216 AspvAlaAspLeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCys 225
Db      701 ACAGTAGATTG---TTGACACCAAAACTTTC-----TGC 733
Qy      236 LysLys-----GlyAspProLysHisGly 243
Db      734 CGGGCTCAGATCTCCATGACACCAACCACTTCTCTTGCAGAGTCACTGATATG 793
Qy      244 LysArgLysArgLysArgProArgLysLeuSerLysGlyLysTrpAspCysLeuGly 263
Db      794 AAAAAGAGAGAAACCCCTGCAAGTGCACACCAAA-----832
Qy      264 LysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeu 283
Db      833 -----AMGACCAACCCGAGAGGAGACTCACTTATGGAAATTCATCCCGACATCTTC 883
Qy      284 IleHisProGluLeuLeuAngLysLysLeuMetLysTrpGluAsnArgHisGlyValPhe 303
Db      884 TTAAACCCAGACAAAGAACCCAGATTAATAAATGGAGACCGATCTGAGGCGTCTTC 943
Qy      304 LysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysAsnSerAsn 323
Db      944 AGGTTCTTGAAATCAGAGGAGTGGCTCACTATGGGCTAAAGAGAGAAACACAGACG 1003
Qy      324 MetThrTrpGluLysLeuSerArgAlaMetArgTrpTrpLysArgGluIleLeuGlu 343
Db      1004 ATGACCTATGAAAGCTCAGCCGACTATGATATTAATAAAGAGAAATATCTGAG 1063
Qy      344 ArgValAspGlyArgArgLysValLysLysPheGlyLysAsnSerSerGlyTrpLysGlu 363
Db      1064 CGGTGTGATGAGCAAGACTGTATATTAATTTGGGAAAGATGCCGAGATGAGAGAA 1123
Qy      364 GluGlu 365
Db      1124 AATGAA 1129

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RESULT 13
US-09-009-913-4

Sequence 4, Application US/0909913
Patent No. 6087485

GENERAL INFORMATION:

APPLICANT: Axy's Pharmaceuticals, Inc.

TITLE OF INVENTION: Asthma Related Genes

NUMBER OF SEQUENCES: 339

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bozicevic & Reed, LLP

STREET: 285 Hamilton Ave, Suite 200

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,913

FILING DATE: 21-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J

REGISTRATION NUMBER: 36,677

REFERENCE/DOCKET NUMBER: SEQ-4P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-327-3231

TELEFAX: 650-327-3231

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/ TELLEX:
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5667 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-09-009-913-4

Alignment Scores:
Pred. No.: 7,22e-46
Score: 555.50
Percent Similarity: 51.24%
Best Local Similarity: 39.13%
Query Match: 28,06%
DB: 3

US-08-978-217-2 (1-371) x US-09-009-913-4 (1-5667)

Qy      59 TrpLeuGlyGluGlnProGlnPheTrpSerLysThrGlnValLeuAspTrpIleSerTrp 78
Db      513 TGGCATGAATTCATCTCAGTACTGTGACCAAGTACAGAGTGGAGTGGCTCCAGCAC 572
Qy      79 GlnValGluLysAsnLysTrpAspAlaSerAlaIleAspPheSerArgCysAspMetAsp 98
Db      573 CTCCTGACCAACCAACCACTGAGTCCATTTGATCCCTTCCAAAGATTGCAATCAAC 632
Qy      99 GlyAlaThrLeuCysAsnLysAlaLeuGluGluLeuValPheGlyProLeuGly 118
Db      633 GCGACACACTCTGACAGATGAGTTTGACAGATTCAACCGGCGGCGGCGGCGGCGG 692
Qy      119 AspGlnLeuHisAlaLeuArgAspLeuThr-----SerSerSerSerAspGlu 135
Db      693 CAGCTCTCTACAGCAACTTGCAGCATCTGAAGTGAACGGCCAGTCAAGTGAAC--- 749
Qy      136 LeuSerTrpIleIleGluLeuLeuGluLysAspGlyMetAlaPheGlnGluAlaLeuAsp 155
Db      750 -----CTGTTCCAGTCC-----761
Qy      156 ProGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGlnGln 175
Db      762 -----ACACAAATGTCATGTCTCAAGACTGAACAA 791
Qy      176 AlaSerProTrpHisProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAsp 195
Db      792 ACTGAGCT-----800
Qy      196 ValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySer 215
Db      801 ---TCCATCATGAACACCTGGAAAGACGAACTATTATATGACACCAACTATGGTAGC 857
Qy      216 AspvAlaAspLeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCys 225
Db      858 ACAGTAGATTG---TTGACACCAAAACTTTC-----TGC 890
Qy      236 LysLys-----GlyAspProLysHisGly 243
Db      991 CGGGCTCAGATCTCCATGACCAACCAACCACTTCTCTTGCAGAGTCACTGATATG 950
Qy      244 LysArgLysArgLysArgProArgLysLeuSerLysGlyLysTrpAspCysLeuGly 263
Db      951 AAAAAGAGAGAAACCCCTGCAAGTGCACACCAAA-----989
Qy      264 LysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeu 283
Db      990 -----AAGACCAACCCGAGAGGAGTCACTTATGGGAATTCATCCGCAATCTTC 1040
Qy      284 IleHisProGluLeuLeuAngLysLysLeuMetLysTrpGluAsnArgHisGlyGlyValPhe 303
Db      1041 TTGAACCCAGACAAAGAACCCAGATTAATAAATGGAGAACCGAATCTGAGGCGTCTTC 1100
Qy      304 LysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsn 323

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Db      1101 AGGTTCTTGAATACAGGAGCGAGTGGCTACCTATAGGGGTAAGAAACAACAGCAGC 1160
Qy      324 MetThrTyrGluTyrLeuSerArgAlaMetArgTyrTyrTyrLeuValIleLeuGlu 343
Db      1161 ATGACCTATATAAAGCTCAGCCGACTATGATATTACTACAAAGAAATTACTGGAG 1220
Qy      344 ArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSerGlyTyrPlyGlu 363
Db      1221 CGTGTGATGACGACGAGCTGTATATAATTGGAAAGATGCCGAGATGGAGAGAA 1280
Qy      364 GluGlu 365
Db      1281 AATGAA 1286

RESULT 14
US-09-020-956-44/C
; Sequence 44, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillion, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 852 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-020-956-44

Alignment Scores:
Pred. No.:      1 86e-43      Length:      852
Score:          519.50      Matches:      121
Percent Similarity: 50.97%      Conservative: 37
Best Local Similarity: 39.03%      Mismatches: 73
Query Match:     26.24%      Indels:    79
DB:              3          Gaps:          8

US-08-978-217-2 (1-371) x US-09-020-956-44 (1-852)
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Db      850 CAGGTGTGGAGAGGCGCTCATCACCTCCTGGACACCAACGAGCGATGGCAATTGTATC 791
Qy      91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCyAsnCyValAlaLeuGluGluLeu 110

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Db      790 CCTTTCANGAGTTGCACATCAACGGCGAGCACCTTTGACAGCTGTGACGGAGTTTC 731
Qy      111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr 129
Db      730 ACCGGGGCGGCGAGGAGCGGGGGCAGNCCTCTTACAGCAACTTGCAGCATCTGAAGTGG 671
Qy      130 -----SerSerSerSerAspGlnLeuSerTyrPleIleGluLeuLeuGluLysAspGly 147
Db      670 AACGGCCAGTGCAGTGTGAC-----
Qy      148 MetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
Db      649 ---CTGTCCAGTCC-----ACACAC 632
Qy      168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCysGlyAlaGly 187
Db      631 AATGTCAATTGTCAAGCTGACAACTGAGCC-----599
Qy      188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSer 207
Db      598 -----TCCATCATGAAACCTCGAAGACNAAACTAT 566
Qy      208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
Db      565 TTATATGACACCACTATGATGACACAGTATGATG-----TTGACACAGCAAACTTTC 512
Qy      228 ProSerAspGlyPheArgAspCysLysLys-----237
Db      511 -----TCCGGGGCTCAGATCTCCATGACACACCACTCACCTT 473
Qy      238 -----GlyAspProLysHisGlyLysValGlyAspGlyArgProArgLysLeuSerLys 255
Db      472 CCTGTTCAGAGTCACCTGATATGAAAGAGCAAGACCCCTCCCAAGTCCACACC 413
Qy      256 GluTyrTrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeu 275
Db      412 AAA-----AACCAACAACCCGAGAGGACTCACTTA 383
Qy      276 TrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluLysLeuMetLysTrp 295
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Qy      296 GluAsnArgHisGluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrp 315
Db      322 GAAGACCGATCTGAGCGCGCTTCAGGTTCTTGAATTCAGAGGCACTGGCTCAGCTATGG 263
Qy      316 GluGlnLysLysLysAsnSerAsnMetTrpTyrGluLysLeuSerArgAlaMetArgTyr 335
Db      262 GGTAAAGAGAGAAACAACAGCACTGATGAAAGCTCAGCCGAGCTATGAGATAT 203
Qy      336 TyrTyrLysArgGluIleLeuGluArgValAspGlyArgArgLeuValTyrLysPheGly 355
Db      202 TACTACAAAAGAAATTTCTGAGCGCTGTGATGAGCAAGACTGTATATAATTGGGG 143
Qy      356 LysAsnSerSerGlyTyrPlyGluGlu 365
Db      142 AAGAAATGCCGAGATGAGAGAAATGAA 113

RESULT 15
US-09-030-607-44/C
; Sequence 44, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillion, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA

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COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427G3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-44

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Alignment Scores:
Pred. No.: 1,86e-43 Length: 852
Score: 519.50 Matches: 121
Percent Similarity: 50.97% Conservative: 37
Best Local Similarity: 39.03% Mismatches: 73
Query Match: 26.24% Indels: 79
DB: 3 Gaps: 8

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US-08-978-217-2 (1-371) x US-09-030-607-44 (1-852)

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QY 91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnGlyAlaLeuGlnLeu 110
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QY 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisIleGlnLeuAspLeuThr--- 129
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QY 130 -----SerSerSerSerSerSerSerSerTrpIleIleGlnLeuGlnLysAspGly 147
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QY 148 MetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlnLysSerProPheAlaGln 167
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QY 168 GlnLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCysGlyAlaGly 187
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Db 631 AATGTCTTTTCAAGACTGACCAAACTGAGCT----- 599

QY 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSer 207
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QY 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
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Db 511 -----TGCCGGGCTCAGATCTCCATGACACCAACGATCACTT 473
QY 238 -----GlyAspProLysHisGlyLysAspGlyAspGlyAspProArgLysLeuSerLys 255
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QY 256 GlnTyrTrpAspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeu 275
   ||||| :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
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QY 276 TrpGlnPheIleArgAspIleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTrp 295
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Db 382 TGGGAATTCATCCGCGACATCTCTTGAACCCAGACCAAGAACCCAGGATTAATAAATGG 323

QY 296 GlnAsnArgHisGlnGlyValPheLysPheLeuArgSerGlnAlaValAlaGlnLeuTrp 315
   ||||| :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 322 GAAGACCGATCTGAGGGCGTCTTCAGGTTCTTGAAATCAGAGGCGTGGCTCAGCTATGG 263

QY 316 GlnGlnLysLysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyr 335
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Db 202 TACTACAAAAGAAATCTCGAGCGTGTGATGACGAAGACTGGTATATTAATTTGGG 143

QY 356 LysAsnSerSerGlyTrpLysGlnGlnGlu 365
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Db 142 AAGAAATGCCGAGATGAGAGAAATGAA 113

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Job time : 127.561 sec

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:42:48 ; Search time 523.407 Seconds
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Title: US-08-978-217-1

Perfect score: 1116
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0
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Maximum Match 100%

Database :

Published Applications NA.*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1116	100.0	1907	15	US-10-291-808-27
3	1116	100.0	1915	9	US-09-964-824A-101
4	1116	100.0	1915	9	US-09-964-824A-563
5	1116	100.0	1915	9	US-09-880-107-3420
6	1116	100.0	1915	9	US-09-967-768A-192
7	1116	100.0	1917	9	US-09-922-217-1105
8	1116	100.0	1917	13	US-10-025-380-1105
9	1115.6	100.0	1956	9	US-09-925-301-207
10	1114.4	99.9	1956	16	US-10-264-049-756
11	933	83.6	2269	15	US-10-131-410-64
12	624.4	55.9	626	9	US-09-922-217-853

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C 14	624.4	55.9	626	13	US-10-025-380-853	Sequence 853, App
C 15	561.4	50.3	563	9	US-09-922-217-944	Sequence 944, App
C 16	561.4	50.3	563	9	US-09-833-263-944	Sequence 944, App
C 17	561.4	50.3	563	13	US-10-025-380-944	Sequence 944, App
C 18	499.4	44.7	502	9	US-09-604-287A-282	Sequence 282, App
C 19	499.4	44.7	502	9	US-09-834-755-282	Sequence 282, App
C 20	499.4	44.7	502	9	US-09-339-338-282	Sequence 282, App
C 21	499.4	44.7	502	10	US-09-551-621-282	Sequence 282, App
C 22	499.4	44.7	502	13	US-10-007-805-282	Sequence 282, App
C 23	499.4	44.7	502	14	US-10-076-632-282	Sequence 282, App
C 24	499.4	44.7	502	15	US-10-124-805-282	Sequence 282, App
C 25	455	40.8	499	9	US-09-998-598-2290	Sequence 2290, App
C 26	372	33.3	437	9	US-09-998-598-2216	Sequence 4818, App
C 27	349	31.3	355	9	US-09-867-701-4818	Sequence 3261, App
C 28	236	21.1	275	14	US-10-060-036-3261	Sequence 32, App
C 29	220	19.7	451	9	US-09-998-598-32	Sequence 1953, App
C 30	159	17.8	1435	15	US-10-017-161-1953	Sequence 1601, App
C 31	199	17.8	1435	15	US-10-292-798-1601	Sequence 11873, A
C 32	175.6	15.7	440	9	US-09-960-352-11873	Sequence 1740, App
C 33	174	15.6	174	9	US-09-998-598-1740	Sequence 1081, App
C 34	173.8	15.6	832	16	US-10-240-425-1081	Sequence 44, App1
C 35	173.8	15.6	852	9	US-09-759-143-44	Sequence 44, App1
C 36	173.8	15.6	852	9	US-09-780-606-44	Sequence 44, App1
C 37	173.8	15.6	852	9	US-09-030-606-44	Sequence 44, App1
C 38	173.8	15.6	852	9	US-09-822-827-44	Sequence 44, App1
C 39	173.8	15.6	852	9	US-09-115-453-44	Sequence 44, App1
C 40	173.8	15.6	852	9	US-09-232-880-44	Sequence 44, App1
C 41	173.8	15.6	852	9	US-09-895-793-44	Sequence 44, App1
C 42	173.8	15.6	852	9	US-09-895-814-44	Sequence 44, App1
C 43	173.8	15.6	852	13	US-10-012-896-44	Sequence 44, App1
C 44	173.8	15.6	852	14	US-10-010-940-44	Sequence 44, App1
C 45	173.8	15.6	852	15	US-10-144-678A-44	Sequence 44, App1

ALIGNMENTS

RESULT 1
US-10-097-340-74
; Sequence 74, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOESRACH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; FILE REFERENCE: Assessment, Prevention, and Therapy of Ovarian Cancer
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732

;; PRIOR FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: 60/325,102
;; PRIOR FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 60/323,580
;; PRIOR FILING DATE: 2001-09-19
;; NUMBER OF SEQ ID NOS: 363
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 74
;; LENGTH: 1907
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-097-340-74

Query Match 100.0%; Score 1116; DB 14; Length 1907;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGCAACCTGTGATTTAGCAATTTTGAACATCTTCACTGGAGTATACAGC 60
DB 96 ATGGCTGCAACCTGTGATTTAGCAATTTTGAACATCTTCACTGGAGTATACAGC 155
QY 61 TCGGAGACTTCACCTGAGCTCTGTTCCTCCCTGCTCCACCTTTGGGGCCGATGACTTG 120
DB 156 TCGGAGACTTCACCTGAGCTCTGTTCCTCCCTGCTCCACCTTTGGGGCCGATGACTTG 215
QY 121 GTAAGTACCTGAGCAACCCCGAGATGTCAATGGAGGTACAGAAAGCCAGCTGGTTG 180
DB 216 GTAAGTACCTGAGCAACCCCGAGATGTCAATGGAGGTACAGAAAGCCAGCTGGTTG 275
QY 181 GGGGAACAGCCCGAGCTTGTGTGCAACAGCGAGTCTTGGACTGATACCTACCAAGTG 240
DB 276 GGGGAACAGCCCGAGCTTGTGTGCAACAGCGAGTCTTGGACTGATACCTACCAAGTG 335
QY 241 GAGAAAGCAAGTACGACGAGGAGCCATGATCTTCAAGATGTGATGATGAGGCGC 300
DB 336 GAGAAAGCAAGTACGACGAGGAGCCATGATCTTCAAGATGTGATGATGAGGCGC 395
QY 301 ACCCTGCAATGTGTGCTTGAAGAGCTGCTGTGCTTTGGGCTCTGGGGAGCA 360
DB 396 ACCCTGCAATGTGTGCTTGAAGAGCTGCTGTGCTTTGGGCTCTGGGGAGCA 455
QY 361 CTCATGCCCCAGCTGCGAGACCTTCACTTCAAGCTCTTGTATGAGCTCACTTGAATAT 420
DB 456 CTCATGCCCCAGCTGCGAGACCTTCACTTCAAGCTCTTGTATGAGCTCACTTGAATAT 515
QY 421 GAGCTGTGAGAAAGATGAGATGAGCTTCCAGAGAGGCCCTTAAGCCAGAGGCCCTTTGAC 480
DB 516 GAGCTGTGAGAAAGATGAGATGAGCTTCCAGAGAGGCCCTTAAGCCAGAGGCCCTTTGAC 575
QY 481 CAGGGAGAGCCCTTTGCGCAAGAGCTGTGACGACGCTGACAGCAAGCCAGCCCTTACAC 540
DB 576 CAGGGAGAGCCCTTTGCGCAAGAGCTGTGACGACGCTGACAGCAAGCCAGCCCTTACAC 635
QY 541 CCGGGAGCTGTGGCGGAGAGAGCCCTCCCTGAGAGCTGTGACGCTCTCAACCGAGGG 600
DB 636 CCGGGAGCTGTGGCGGAGAGAGCCCTCCCTGAGAGCTGTGACGCTCTCAACCGAGGG 695
QY 601 ACTGATGCTTCTCGAGAGCTCCCACTCTCAAGACTCCGAGTGAAGTACGATGAGAT 660
DB 696 ACTGATGCTTCTCGAGAGCTCCCACTCTCAAGACTCCGAGTGAAGTACGATGAGAT 755
QY 661 CCGCATGATGAGCAAGCTTTCCCGAGAGTGTGTTTGTGATGCTCAAGAAAGGGGATCCC 720
DB 756 CCGCATGATGAGCAAGCTTTCCCGAGAGTGTGTTTGTGATGCTCAAGAAAGGGGATCCC 815
QY 721 AAGCAGCGGAGCGGAAACGAGGCGGAGCCCGGAAAGCTGAGCAAGAGTACTGAGACTGT 780
DB 816 AAGCAGCGGAGCGGAAACGAGGCGGAGCCCGGAAAGCTGAGCAAGAGTACTGAGACTGT 875
QY 781 CTGAGGCGGAGAAAGACAGCAAGCGGCGGAGAGGCAACCACTGTGGAGTTCAATCCGG 840
DB 876 CTGAGGCGGAGAAAGACAGCAAGCGGCGGAGAGGCAACCACTGTGGAGTTCAATCCGG 935

QY 841 GACATCTCATCCACCCGAGCTCAACGAGGCGCTCATGATGAGAGATGGCATGAA 900
DB 936 GACATCTCATCCACCCGAGCTCAACGAGGCGCTCATGATGAGAGATGGCATGAA 995
QY 901 GGGCTCTTAAGTCTCTGGGCTCCGAGGCTGTGGGCCCACTATGGGGCCAAAAGAAAAG 960
DB 996 GGGCTCTTAAGTCTCTGGGCTCCGAGGCTGTGGGCCCACTATGGGGCCAAAAGAAAAG 1055
QY 961 AACGCAAGATGACCTTACAGAAAGCTGAGCCGAGCCATGAGTACTTACTACAAACGGAG 1020
DB 1056 AACGCAAGATGACCTTACAGAAAGCTGAGCCGAGCCATGAGTACTTACTACAAACGGAG 1115
QY 1021 ATCTGTAACGGGTGATGAGCGCGGAGCTGCTTCAAGATTTGGCAAAAACCTCAAGCGC 1080
DB 1116 ATCTGTAACGGGTGATGAGCGCGGAGCTGCTTCAAGATTTGGCAAAAACCTCAAGCGC 1175
QY 1081 TGGAGAGAGAGAGTCTCCAGAGTCCGAACTGA 1116
DB 1176 TGGAGAGAGAGAGTCTCCAGAGTCCGAACTGA 1211

RESULT 2

US-10-291-808-27
;; Sequence 27, Application US/10291808
;; Publication No. US20030224382A1
;; GENERAL INFORMATION:
;; APPLICANT: McCelland, Michael
;; APPLICANT: Welsh, John
;; APPLICANT: Trenkle, Thomas
;; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
;; FILE REFERENCE: P-PH 3457
;; CURRENT APPLICATION NUMBER: US/10/291,808
;; PRIOR FILING DATE: 2002-11-07
;; PRIOR APPLICATION NUMBER: US/09/300,958
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/083,331
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: 60/098,070
;; PRIOR FILING DATE: 1998-08-27
;; PRIOR APPLICATION NUMBER: 60/118,624
;; PRIOR FILING DATE: 1999-02-04
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 27
;; LENGTH: 1907
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-291-808-27

Query Match 100.0%; Score 1116; DB 15; Length 1907;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGCAACCTGTGATTTAGCAATTTTGAACATCTTCACTGGAGTATACAGC 60
DB 96 ATGGCTGCAACCTGTGATTTAGCAATTTTGAACATCTTCACTGGAGTATACAGC 155
QY 61 TCGGAGACTTCACCTGAGCTCTGTTCCTCCCTGCTCCACCTTTGGGGCCGATGACTTG 120
DB 156 TCGGAGACTTCACCTGAGCTCTGTTCCTCCCTGCTCCACCTTTGGGGCCGATGACTTG 215
QY 121 GTAAGTACCTGAGCAACCCCGAGATGTCAATGGAGGTACAGAAAGCCAGCTGGTTG 180
DB 216 GTAAGTACCTGAGCAACCCCGAGATGTCAATGGAGGTACAGAAAGCCAGCTGGTTG 275
QY 181 GGGGAACAGCCCGAGCTTGTGTGCAACAGCGAGTCTTGGACTGATCAGTACCAAGTG 240
DB 276 GGGGAACAGCCCGAGCTTGTGTGCAACAGCGAGTCTTGGACTGATCAGTACCAAGTG 335
QY 241 GAGAAAGCAAGTACGACGAGGAGCCATGATCTTCAAGATGTGATGATGAGGCGC 300
DB 336 GAGAAAGCAAGTACGACGAGGAGCCATGATCTTCAAGATGTGATGATGAGGCGC 395

QY 301 ACCCTGCAATTGTCCTTGAGAGCTGCGCTGTGCTTTGGGCTCTGCGGAGCA 360
 DB 396 ACCCTGCAATTGTCCTTGAGAGCTGCGCTGTGCTTTGGGCTCTGCGGAGCA 455
 QY 361 CTCATGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 456 CTCATGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 515
 QY 421 GAGCTCTGAG 480
 DB 516 GAGCTCTGAG 575
 QY 481 GAGGAG 540
 DB 576 GAGGAG 635
 QY 541 CCGGAG 600
 DB 636 CCGGAG 695
 QY 601 ACTGAG 660
 DB 696 ACTGAG 755
 QY 661 CCGAG 720
 DB 756 CCGAG 815
 QY 721 AAGCAG 780
 DB 816 AAGCAG 875
 QY 781 CTCGAG 840
 DB 876 CTCGAG 935
 QY 841 GACATCTCATCCAG 900
 DB 936 GACATCTCATCCAG 995
 QY 901 GGGGCTTCAAGTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 DB 996 GGGGCTTCAAGTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1055
 QY 961 AAGCAG 1020
 DB 1056 AAGCAG 1115
 QY 1021 ATCTGAG 1080
 DB 1116 ATCTGAG 1175
 QY 1081 TGAAG 1116
 DB 1176 TGAAG 1211
 RESULT 3
 US-09-964-824A-101
 ; Sequence 101, Application US/09964824A
 ; Patent No. US20020102531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horrigan, Stephen
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
 ; TITLE OF INVENTION: Sets
 ; FILE REFERENCE: 689290-73
 ; CURRENT APPLICATION NUMBER: US/09/964, 824A
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US/60/236, 033
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236, 032
 ; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236, 028
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 583
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 101
 ; LENGTH: 1915
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-964-824A-101
 Query Match 100.0%; Score 1116; DB 9; Length 1915;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCTGCAACCTGAGATTGAGCAATTTTACCACTTCTAGTGCATGTACAGC 60
 DB 120 ATGGCTGCAACCTGAGATTGAGCAATTTTACCACTTCTAGTGCATGTACAGC 179
 QY 61 TCGAGAGACTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 DB 180 TCGAGAGACTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239
 QY 121 GTACTGACCTTGAAGCAACCCAGATGATTTGAGAGGTTACAGAGAGGCTGCTG 180
 DB 240 GTACTGACCTTGAAGCAACCCAGATGATTTGAGAGGTTACAGAGAGGCTGCTG 299
 QY 181 GGGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 DB 300 GGGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359
 QY 241 GAGAGAGCAAGTACAGACGCAAGCGCATTTGACTTCTCAGATGTGACATGATGCGGC 300
 DB 360 GAGAGAGCAAGTACAGACGCAAGCGCATTTGACTTCTCAGATGTGACATGATGCGGC 419
 QY 301 ACCCTGCAATTGTCCTTGAGAGCTGCGCTGTGCTTTGGGCTCTGCGGAGCA 360
 DB 420 ACCCTGCAATTGTCCTTGAGAGCTGCGCTGTGCTTTGGGCTCTGCGGAGCA 479
 QY 361 CTCATGAGGAG 420
 DB 480 CTCATGAGGAG 539
 QY 421 GAGCTCTGAG 480
 DB 540 GAGCTCTGAG 599
 QY 481 CAGGAG 540
 DB 600 CAGGAG 659
 QY 541 CCGGAG 600
 DB 660 CCGGAG 719
 QY 601 ACTGAG 660
 DB 720 ACTGAG 779
 QY 661 CCGCAG 720
 DB 780 CCGCAG 839
 QY 721 AAGCAG 780
 DB 840 AAGCAG 899
 QY 781 CCGAG 840
 DB 900 CCGAG 959
 QY 841 GACATCTCATCCAG 900
 DB 960 GACATCTCATCCAG 1019

QY	901	GGCGCTTCAAGTTCCTGGCGCTCCAGAGGTGGGCCCAACTATTTGGGGCCAAAAGAAAAG	960
Db	1020	GGCGCTTCAAGTTCCTGGCGCTCCAGAGGTGGGCCCAACTATTTGGGGCCAAAAGAAAAG	1078
QY	961	AACAGCAACATGACCTACGAGAAAGCTGAGCCGGGCGCATGAGGTACTACTCAACCGGAG	1020
Db	1080	AACAGCAACATGACCTACGAGAAAGCTGAGCCGGGCGCATGAGGTACTACTCAACCGGAG	1138
QY	1021	ATCTCGGAAACGGGTGGATGGCCGGGGGACTCTGCTCTCAAGTTTGGCAAAAACCTCAAGCGGC	1088
Db	1140	ATCTCGGAAACGGGTGGATGGCCGGGGGACTCTGCTCTCAAGTTTGGCAAAAACCTCAAGCGGC	1196
QY	1081	TGGAAGAGAGAAAGAGTTCCTCAGAGTCCGAACTGA	1116
Db	1200	TGGAAGAGAGAAAGAGTTCCTCAGAGTCCGAACTGA	1235

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RESULT 4
US-09-964-824A-563
: Sequence 563: Application US/09964822A
: Patent No. US20020102531A1
: GENERAL INFORMATION:
: APPLICANT: Horrigan, Stephen
: TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
: TITLE OF INVENTION: Sets
: FILE REFERENCE: 689290-73
: CURRENT APPLICATION NUMBER: US/09/964,824A
: CURRENT FILING DATE: 2001-09-27
: PRIOR APPLICATION NUMBER: US/60/236,033
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US/60/236,032
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US/60/236,028
: PRIOR FILING DATE: 2000-09-28
: NUMBER OF SEQ ID NOS: 583
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 563
: LENGTH: 1915
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-964-824A-563

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Query Match	100.0%;	Score 1116;	DB 9;	Length 1915;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 116;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	ATGGTGGAACTGGAGATTAGCAACATTTTACACACTTATAGTGGCGATGACAGC	60
Db	120 ATGGCTGCACACTGTGAGATTGCAACAATTTTATCAACTACTTACGTGCATGTACAGC	179
QY	61 TCGAGGACTCCACCCTGGCCCTGTGTCCCTCGTGGCACTTTGGGGCCGATGACATTG	120
Db	180 TCGAGGAGCTCCACCCTGGCCCTGTGTCCCTCGTGGCACTTTGGGGCCGATGACATTG	239
QY	121 GTACTGACCTTGAGCAACCCCCAGATGTCAATTGAGGGGTACAGAAAGCCAGCTGGTTG	180
Db	240 GTACTGACCTTGAGCAACCCCCAGATGTCAATTGAGGGGTACAGAAAGCCAGCTGGTTG	299
QY	181 GGGGAAACGCCCCAGTTCTGTGTCAAGACGACAGTTCTGGACTGGAATCACTTCCAACTG	240
Db	300 GGGGAAACGCCCCAGTTCTGTGTCAAGACGACAGTTCTGGAATCACTTCCAACTG	359
QY	241 GAGAAAGACAAGTACGACGCAAGCCATTGACTTCAACGATGTGACATGGATGGCCGC	300
Db	360 GAGAAAGACAAGTACGACGCAAGCCCATTTGACTTCAACGATGTGACATGGATGGCCGC	419
QY	301 ACCCTCTGCAATTGTGCCCTTGAGAGCTGCGTCTTGTTGGGCTCTGGGGAGCCAA	360
Db	420 ACCCTCTGCAATTGTGCCCTTGAGAGCTGCGTCTTGTTGGGCTCTGGGGAGCCAA	479
QY	361 CTCATGCCCAAGCTGAGACCTTCACTTCCAGCTCTTCTGATGAGCTCAATTGATCAATT	420

Db	480	CTCCATGCGCCAGCTGCGAGAACCTCACTTCCAGCTCTTCTGATGAGCTCAGTTGGATCA	539
Oy	421	GAGCTGCTGGAGGAAGATGGATGGCTTTCAGAGAGGCCCTTAAGACCCAGGGCCCTTTGAC	480
Db	540	GAGTGTCTGGAGGAAGATGGATGGCTTTCAGAGAGGCCCTTAAGACCCAGGGCCCTTTGAC	599
Oy	481	CAGGGCAGACCCTTTGGCCAGAGAGCTGTGGACAGACGGTCAGCAAGCCAGCCCTTACAC	540
Db	600	CAGGGCAGACCCTTTGGCCAGAGAGCTGTGGACAGACGGTCAGCAAGCCAGCCCTTACAC	659
Oy	541	CCCGGAGAGCTGTGGCGAGAGAGCCCTCTCCCTGGAGCTTGAAGTCTCCACCGCAGGG	600
Db	660	CCCGGAGAGCTGTGGCGAGAGAGCCCTCTCCCTGGAGCTTGAAGTCTCCACCGCAGGG	719
Oy	601	ACTGGTGCTTCTGGAGAGCTCCCACTCTCAGACTCCGGTGGAAAGTGAAGCTGAGTCTGAT	660
Db	720	ACTGGTGCTTCTGGAGAGCTCCCACTCTCAGACTCCGGTGGAAAGTGAAGCTGAGTCTGAT	779
Oy	661	CCCACTGATGGCAGAGCTTTCCCAAGAGATGGTTTGGTGACTGCAAGAGGGGGATCCC	720
Db	780	CCCACTGATGGCAGAGCTTTCCCAAGAGATGGTTTGGTGACTGCAAGAGGGGGATCCC	839
Oy	721	AAGCAGCGGGAAGCGGAACGAGGCCCGGCCGGAAGCTGAGCAAAAGTACTGGGACTGT	780
Db	840	AAGCAGCGGGAAGCGGAACGAGGCCCGGCCGGAAGCTGAGCAAAAGTACTGGGACTGT	899
Oy	781	CTCGAGGGCAAGAGAGCAGACGCGCCAGAGGACCCACTCTGTGGAGTTCA	840
Db	900	CTCGAGGGCAAGAGAGCAGACGCGCCAGAGGACCCACTCTGTGGAGTTCA	959
Oy	841	GACATCTCTCAATCCACCCGGAGCTCAAGAGGGGCTCTAGAAAGTGGGAAGATCGGCATGAA	900
Db	960	GACATCTCTCAATCCACCCGGAGCTCAAGAGGGGCTCTAGAAAGTGGGAAGATCGGCATGAA	1019
Oy	901	GGCGTCTTCAAGTCTCTGCGCTCGAGAGCTGTGGCCCAACTATGAGGCGCAAAAGAAAG	960
Db	1020	GGCGTCTTCAAGTCTCTGCGCTCGAGAGCTGTGGCCCAACTATGAGGCGCAAAAGAAAG	1079
Oy	961	AACAGCAACATGACCTTACGAGAGCTGAGCCGGGCCATGAGATCTACTCAACACGGGAG	1020
Db	1080	AACAGCAACATGACCTTACGAGAGCTGAGCCGGGCCCATGAGATCTACTCAACACGGGAG	1139
Oy	1021	ATCTCTGGAACGGGTGGATGGCCGGCCGACTGTCATCAAGTTTGGCAAAAATCTCAAGGGC	1080
Db	1140	ATCTCTGGAACGGGTGGATGGCCGGCCGACTGTCATCAAGTTTGGCAAAAATCTCAAGGGC	1199
Oy	1081	TGGAAGAGGAAGAGTTCTTCCAGAGTCGGAACCTGA	1116
Db	1200	TGGAAGAGGAAGAGTTCTTCCAGAGTCGGAACCTGA	1235

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RESULT 5
US-09-880-107-3420
: Sequence 3420, Application US/09880107
: Patent No. US20020142981A1
: GENERAL INFORMATION:
: APPLICANT: Horne, Darci T.
: APPLICANT: Vockley, Joseph G.
: APPLICANT: Scheer, Uwe
: APPLICANT: Gene Logic, Inc.
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
: FILE REFERENCE: 44921-5028-WO
: CURRENT APPLICATION NUMBER: US/09/880,107
: PRIORITY FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/237,054
: PRIOR FILING DATE: 2000-10-02
: NUMBER OF SEQ ID NOS: 3950
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3420
: LENGTH: 1915
: TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843
US-09-880-107-3420

Query Match      100.0%; Score 1116; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGCAACCTGTGAGATTAGCAATTTTATAGCACTACTTCACTTGTGAGATGATACAGC 60
DB 120 ATGGCTGCAACCTGTGAGATTAGCAATTTTATAGCACTACTTCACTTGTGAGATGATACAGC 179
QY 61 TCGAGAGACTCCACCCCTGCTGTGCTCCCTGCTGCTGCACTTTGAGGCGCATGACTTG 120
DB 180 TCGAGAGACTCCACCCCTGCTGTGCTCCCTGCTGCTGCACTTTGAGGCGCATGACTTG 239
QY 121 GTAATGACCTTGAGCAACCCCGATGTCATTTGAGAGGTA CAGAGAGCCAGCTGGTTG 180
DB 240 GTAATGACCTTGAGCAACCCCGATGTCATTTGAGAGGTA CAGAGAGCCAGCTGGTTG 239
QY 181 GGGGAAACGCCCCAGTTCTGTGTAAGACGCAAGTTCTGATGATGATCACTACCAAGTG 240
DB 300 GGGGAAACGCCCCAGTTCTGTGTAAGACGCAAGTTCTGATGATGATCACTACCAAGTG 359
QY 241 GAGAGAAAGAAATGACGAGAGGCAATTTGACTTTCAGAGTGTGATGATGAGGCGC 300
DB 360 GAGAGAAAGAAATGACGAGAGGCAATTTGACTTTCAGAGTGTGATGATGAGGCGC 419
QY 301 ACCCTGCAATTTGTGCTTGTGAGAGAGCTGCTGTGCTTTTGGGCTCTGGGGACCA 360
DB 420 ACCCTGCAATTTGTGCTTGTGAGAGAGCTGCTGTGCTTTTGGGCTCTGGGGACCA 479
QY 361 CTCCTATGCCAGCTGCGAGACCTTCACTTCCAGCTTTCTGATGATGATGATGATGAT 420
DB 480 CTCCTATGCCAGCTGCGAGACCTTCACTTCCAGCTTTCTGATGATGATGATGATGAT 539
QY 421 GAGCTGTGAGAGAGATGAGATGAGCTTTCAGAGAGGCGCTTACAGGAGCCCTTTGAC 480
DB 540 GAGCTGTGAGAGAGATGAGATGAGCTTTCAGAGAGGCGCTTACAGGAGCCCTTTGAC 599
QY 481 CAGGAGCAGCCCTTTTGGCCAGAGCTGTGAGACGAGTGAAGCAGAGCCCTTACAC 540
DB 600 CAGGAGCAGCCCTTTTGGCCAGAGCTGTGAGACGAGTGAAGCAGAGCCCTTACAC 659
QY 541 CCGGAGCTGTGCGAGAGAGCCCTTCCCTGCGAGCTTGTGAGCTTCTTCCACCGCAGG 600
DB 660 CCGGAGCTGTGCGAGAGAGCCCTTCCCTGCGAGCTTGTGAGCTTCTTCCACCGCAGG 719
QY 601 ACTGATGCTTCTGAGAGCTCCCACTCTTCAAGACTCCGATGAGAGTGAAGTGAAGCTGAT 660
DB 720 ACTGATGCTTCTGAGAGCTCCCACTCTTCAAGACTCCGATGAGAGTGAAGTGAAGCTGAT 779
QY 661 CCACTATGAGCAAGCTTTTCCCAAGATGATTTTGTGATGCTGCAAGAGGAGATCCC 720
DB 780 CCACTATGAGCAAGCTTTTCCCAAGATGATTTTGTGATGCTGCAAGAGGAGATCCC 839
QY 721 AAGCAGGAGAGCGGAAACGAGCGGCGCCGAAAGCTGAGCAAAAGTACTGAGACTGT 780
DB 840 AAGCAGGAGAGCGGAAACGAGCGGCGCCGAAAGCTGAGCAAAAGTACTGAGACTGT 899
QY 841 CTGAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 900 CTGAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959
QY 841 GACATCTCTATCCACCGGAGCTCAAGAGGCTTCAATGAAGTGGAGAAATCGGCATGAA 900
DB 960 GACATCTCTATCCACCGGAGCTCAAGAGGCTTCAATGAAGTGGAGAAATCGGCATGAA 1019
QY 901 GGGCTTTTCAAGTTCTGCGCTCCGAGGCTGTGAGCTTATGAGGCTCAAAAGAAAAG 960
DB 1020 GGGCTTTTCAAGTTCTGCGCTCCGAGGCTGTGAGCTTATGAGGCTCAAAAGAAAAG 1079
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QY 961 AACAGCAATGACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 1080 AACAGCAATGACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1139
QY 1021 ATCTTGGAACGGGTGATGAGCGGCGGACCTGCTCAATTTTGGCAAAATCAAGCGAG 1080
DB 1140 ATCTTGGAACGGGTGATGAGCGGCGGACCTGCTCAATTTTGGCAAAATCAAGCGAG 1199
QY 1081 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1200 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1235

RESULT 6
US-09-967-768A-192
; Sequence 192, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967, 768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: Patent version 3.0
; SEQ ID NO 192
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-967-768A-192

Query Match      100.0%; Score 1116; DB 9; Length 1915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGCAACCTGTGAGATTAGCAATTTTATAGCACTACTTCACTTGTGAGATGATACAGC 60
DB 120 ATGGCTGCAACCTGTGAGATTAGCAATTTTATAGCACTACTTCACTTGTGAGATGATACAGC 179
QY 61 TCGAGAGACTCCACCCCTGCTGTGCTCCCTGCTGCTGCACTTTGAGGCGCATGACTTG 120
DB 180 TCGAGAGACTCCACCCCTGCTGTGCTCCCTGCTGCTGCACTTTGAGGCGCATGACTTG 239
QY 121 GTAATGACCTTGAGCAACCCCGATGTCATTTGAGAGGTA CAGAGAGCCAGCTGGTTG 180
DB 240 GTAATGACCTTGAGCAACCCCGATGTCATTTGAGAGGTA CAGAGAGCCAGCTGGTTG 239
QY 181 GGGGAAACGCCCCAGTTCTGTGTAAGACGCAAGTTCTGATGATGATCACTACCAAGTG 240
DB 300 GGGGAAACGCCCCAGTTCTGTGTAAGACGCAAGTTCTGATGATGATCACTACCAAGTG 359
QY 241 GAGAGAAAGAAATGACGAGAGGCAATTTGACTTTCAGAGTGTGATGATGAGGCGC 300
DB 360 GAGAGAAAGAAATGACGAGAGGCAATTTGACTTTCAGAGTGTGATGATGAGGCGC 419
QY 301 ACCCTGCAATTTGTGCTTGTGAGAGAGCTGCTGTGCTTTTGGGCTCTGGGGACCA 360
DB 420 ACCCTGCAATTTGTGCTTGTGAGAGAGCTGCTGTGCTTTTGGGCTCTGGGGACCA 479
QY 361 CTCCTATGCCAGCTGCGAGACCTTCACTTCCAGCTTTCTGATGATGATGATGATGATGAT 420
DB 480 CTCCTATGCCAGCTGCGAGACCTTCACTTCCAGCTTTCTGATGATGATGATGATGATGAT 539
QY 421 GAGCTGTGAGAGAGATGAGATGAGCTTTCAGAGAGGCGCTTACAGGAGCCCTTTGAC 480
DB 540 GAGCTGTGAGAGAGATGAGATGAGCTTTCAGAGAGGCGCTTACAGGAGCCCTTTGAC 599
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QY 481 CAGGGAGCCCTTTGGCCAGAGCTGTGACGACGGTCAAGCAGCCCTTACAC 540
DB 600 CAGGGAGCCCTTTGGCCAGAGCTGTGACGACGGTCAAGCAGCCCTTACAC 659
QY 541 CCGGCGAGCTGTGGCGAGAGGCCCCCTCCCTGGGAGCTCTACGCTCTCAACCGAGGG 600
DB 660 CCGGCGAGCTGTGGCGAGAGGCCCCCTCCCTGGGAGCTCTACGCTCTCAACCGAGGG 719
QY 601 ACTGATGCTCTGCGAGCTCCCACTCTCAGACTCCGGTGAAGTGAAGTGAAGTGAAGT 660
DB 720 ACTGATGCTCTGCGAGCTCCCACTCTCAGACTCCGGTGAAGTGAAGTGAAGTGAAGT 779
QY 661 CCGAGTATGAGCAAGCTCTTCCCAAGGATGTTTGTGAATGCAAGAAAGGGGATCCC 720
DB 780 CCGAGTATGAGCAAGCTCTTCCCAAGGATGTTTGTGAATGCAAGAAAGGGGATCCC 839
QY 721 AACGAGGGAAGGGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
DB 840 AACGAGGGAAGGGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 899
QY 781 CTCGAGGGAAGGGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
DB 900 CTCGAGGGAAGGGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 959
QY 841 GACATCTCTCAATCCAGCCGAGCTCAACGAGGGCTCATGAATGGGAGAAATCCGATGAA 900
DB 960 GACATCTCTCAATCCAGCCGAGCTCAACGAGGGCTCATGAATGGGAGAAATCCGATGAA 1019
QY 901 GGGGCTCTCAATCCAGCCGAGCTCAACGAGGGCTCATGAATGGGAGAAATCCGATGAA 960
DB 1020 GGGGCTCTCAATCCAGCCGAGCTCAACGAGGGCTCATGAATGGGAGAAATCCGATGAA 1079
QY 961 AACGAGCAATGAGCTCTCAAGAGCTGAGCGGGCGATGAGTACTACTCAAAACGGAG 1020
DB 1080 AACGAGCAATGAGCTCTCAAGAGCTGAGCGGGCGATGAGTACTACTCAAAACGGAG 1139
QY 1021 ATCTGAGCAAGGAGTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
DB 1140 ATCTGAGCAAGGAGTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1199
QY 1081 TGAAGAGGAGGAGGTTCTCCAGAGTCGGAACCTGA 1116
DB 1200 TGAAGAGGAGGAGGTTCTCCAGAGTCGGAACCTGA 1235

RESULT 7
US-09-922-217-1105
Sequence 1105, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeline Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yudi
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922.217
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1105
LENGTH: 1917
TYPE: DNA

ORGANISM: Homo sapiens
US-09-922-217-1105
Query Match 100.0%; Score 1116; DB 9; Length 1917;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTGCAACCTGTGAGATTAGCAATTTTATGCACTTCTAGTGCATGTACAC 60
DB 122 ATGGCTGCAACCTGTGAGATTAGCAATTTTATGCACTTCTAGTGCATGTACAC 181
QY 61 TCGGAGAGCTCCACCTTGGGCTCTGTCTCCCTGCTGCGACCTTTGGGCGGATGACTTG 120
DB 182 TCGGAGAGCTCCACCTTGGGCTCTGTCTCCCTGCTGCGACCTTTGGGCGGATGACTTG 241
QY 121 GTACTGACCTTGAGCAACCCCGAGATGATGATGAGAGGTAGAGAGAGCCAGCTGTTG 180
DB 242 GTACTGACCTTGAGCAACCCCGAGATGATGATGAGAGGTAGAGAGAGCCAGCTGTTG 301
QY 181 GGGGAACAGCCCGAGTTCTGTGTGAAAGACGAGGTTCTGAGCTGATCACTTCAAGTG 240
DB 302 GGGGAACAGCCCGAGTTCTGTGTGAAAGACGAGGTTCTGAGCTGATCACTTCAAGTG 361
QY 241 GAGAAGAACAGTACGACCGGAGCTTGAATCTTCAAGATGATGATGATGAGGCGG 300
DB 362 GAGAAGAACAGTACGACCGGAGCTTGAATCTTCAAGATGATGATGATGAGGCGG 421
QY 301 ACCCTGTGCAATTTGTGCTTGTGAGAGCTGCGTCTGTGAGGCTCTGAGGAGACCAA 360
DB 422 ACCCTGTGCAATTTGTGCTTGTGAGAGCTGCGTCTGTGAGGCTCTGAGGAGACCAA 481
QY 361 CTCATGCTCCAGCTGAGAGCTCACTTCAAGCTCTTGTATGAGCTCACTTGTATGAT 420
DB 482 CTCATGCTCCAGCTGAGAGCTCACTTCAAGCTCTTGTATGAGCTCACTTGTATGAT 541
QY 421 GAGCTGTGAGAGAGGATGAGGATGAGGCTTCCAGAGGCGCTTGAACCAAGGCGCTTGA 480
DB 542 GAGCTGTGAGAGAGGATGAGGATGAGGCTTCCAGAGGCGCTTGAACCAAGGCGCTTGA 601
QY 481 CAGGGAGCCCTTTGGCCAGAGCTGTGAGAGAGCTGTGAGAGAGCTGTGAGAGAGCTGTGAG 540
DB 602 CAGGGAGCCCTTTGGCCAGAGCTGTGAGAGAGCTGTGAGAGAGCTGTGAGAGAGCTGTGAG 661
QY 541 CCGGCGAGCTGTGGCGAGAGGCCCCCTCCCTGGGAGCTTGAAGCTTTCACCCGAGGG 600
DB 662 CCGGCGAGCTGTGGCGAGAGGCCCCCTCCCTGGGAGCTTGAAGCTTTCACCCGAGGG 721
QY 601 ACTGATGCTCTGCGAGCTCCCACTCTCAGACTCCGGTGAAGTGAAGTGAAGTGAAGT 660
DB 722 ACTGATGCTCTGCGAGCTCCCACTCTCAGACTCCGGTGAAGTGAAGTGAAGTGAAGT 781
QY 661 CCGAGTATGAGCAAGCTCTTCCCAAGCGATGTTTGTGATGTCAGAAAGGAGGATCCC 720
DB 782 CCGAGTATGAGCAAGCTCTTCCCAAGCGATGTTTGTGATGTCAGAAAGGAGGATCCC 841
QY 721 AACGAGGGAAGGGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
DB 842 AACGAGGGAAGGGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 901
QY 781 CTCGAGGGAAGGGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
DB 902 CTCGAGGGAAGGGAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 961
QY 841 GACATCTCTATCCACCGGAGCTCAACGAGGCGCTCATGATGAGAGATGAGATGAGATGAG 900
DB 962 GACATCTCTATCCACCGGAGCTCAACGAGGCGCTCATGATGAGAGATGAGATGAGATGAG 1021
QY 901 GGGGCTTCAAGTTCTGTGGCTTCCAGAGCTGTGGCCCACTATGAGGCGCAAAAGAAAG 960
DB 1022 GGGGCTTCAAGTTCTGTGGCTTCCAGAGCTGTGGCCCACTATGAGGCGCAAAAGAAAG 1081
QY 961 AACGAGCAATGAGCTTCAAGAGAGCTGAGCCGGGCGCATGAGTACTATCAAAACGGAG 1020

Db 1082 AACGACAATGAGCTAGAGAAAGTGGCCGGCCATGAGTACTACTACAAACGGAG 1141
Qy 1021 ATCTGGAAGAGGTGATGGCCCGGCACTGCTACAAAGTTTGGCAAAACTAAAGCGC 1080
Db 1142 ATCTGGAAGAGGTGATGGCCCGGCACTGCTACAAAGTTTGGCAAAACTAAAGCGC 1201
Qy 1081 TGGAGAGAGAGAGGTTCTCCAGAGTCGGAAGTGA 1116
Db 1202 TGGAGAGAGAGAGGTTCTCCAGAGTCGGAAGTGA 1237

RESULT 8

US-10-025-380-1105.
; Sequence 1105, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-1105

Query Match 100.0%; Score 1116; DB 13; Length 1917;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTGCAACCTGTGATGATTAACAATTTTACGAACCTACTTCACTGGATGTACAGC 60
Db 122 ATGGCTGCAACCTGTGATGATTAACAATTTTACGAACCTACTTCACTGGATGTACAGC 181
Qy 61 TCGGAGAGCTCAACCTGAGCTGTCTGTTCCCTGCTGCACTTTGGGGCCGATGACTTG 120
Db 182 TCGGAGAGCTCAACCTGAGCTGTCTGTTCCCTGCTGCACTTTGGGGCCGATGACTTG 241
Qy 121 GATGTAACCTGAGCAACCCCAAGATGATTTGAGAGGTACAGAGAAAGCCAGCTGTTG 180
Db 242 GATGTAACCTGAGCAACCCCAAGATGATTTGAGAGGTACAGAGAAAGCCAGCTGTTG 301
Qy 181 GGGGAAACAGCCCAAGTTCTGAGTGAAGAGCAAGTCTGAGACGTGACACTCAAGTG 240
Db 302 GGGGAAACAGCCCAAGTTCTGAGTGAAGAGCAAGTCTGAGACGTGACACTCAAGTG 361
Qy 241 GAGAGAAACAGTACAGAGCAAGCCAGTGAATCTTCAAGATGTGACATGATGGCGC 300
Db 362 GAGAGAAACAGTACAGAGCAAGCCAGTGAATCTTCAAGATGTGACATGATGGCGC 421
Qy 301 ACCCTCTGCAATTTGCTTGAAGAGCTGCTGCTTTTGGGCTCTGGGGGACCAA 360
Db 422 ACCCTCTGCAATTTGCTTGAAGAGCTGCTGCTTTTGGGCTCTGGGGGACCAA 481

Qy 361 CTCATGCCCAGCTGCGAGACCTCACTTCAGCTCTTGTGATGAGCTCAGTTGATCAT 420
Db 482 CTCATGCCCAGCTGCGAGACCTCACTTCAGCTCTTGTGATGAGCTCAGTTGATCAT 541
Qy 421 GAGCTCTGAGAGAGATGAGCTGCTTCCAGAGAGCCCTTAGACCCAGGCTCTTGAC 480
Db 542 GAGCTCTGAGAGAGATGAGCTGCTTCCAGAGAGCCCTTAGACCCAGGCTCTTGAC 601
Qy 481 CAGGAGAGCCCTTGTGAGAGCTGCTGAGACGATGAGAGAGAGAGAGAGAGAGAG 540
Db 602 CAGGAGAGCCCTTGTGAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661
Qy 541 CCGGAGAGCTGAG 600
Db 662 CCGGAGAGCTGAG 721
Qy 601 ACTGAGCTTCTGAGAGCTCCCACTCTGAGACTCCGAGAGAGAGAGAGAGAGAGAG 660
Db 722 ACTGAGCTTCTGAGAGCTCCCACTCTGAGACTCCGAGAGAGAGAGAGAGAGAGAG 781
Qy 661 CCGACTGATGAG 720
Db 782 CCGACTGATGAG 841
Qy 721 AAGCAGGAG 780
Db 842 AAGCAGGAG 901
Qy 781 CTGAG 840
Db 902 CTGAG 961
Qy 841 GATATCTCATCAACCCGAGAGCTCAACGAGAGCTTATGAGAGAGAGAGAGAGAGAG 900
Db 962 GATATCTCATCAACCCGAGAGCTCAACGAGAGCTTATGAGAGAGAGAGAGAGAGAG 1021
Qy 901 GGGCTCTTCAAGTTCTGAGCTCCGAGAGCTGAGAGCTGAGAGCTGAGAGAGAGAG 960
Db 1022 GGGCTCTTCAAGTTCTGAGCTCCGAGAGCTGAGAGCTGAGAGCTGAGAGAGAGAG 1081
Qy 961 AACGACAATGAGCTTACGAGAGAGCTGAGCCGGGCCATGAGGTACTTACAAACGGAG 1020
Db 1082 AACGACAATGAGCTTACGAGAGAGCTGAGCCGGGCCATGAGGTACTTACAAACGGAG 1141
Qy 1021 ATCTGGAAGAGGTGATGGCCCGGCACTGCTACAAAGTTTGGCAAAACTAAAGCGC 1080
Db 1142 ATCTGGAAGAGGTGATGGCCCGGCACTGCTACAAAGTTTGGCAAAACTAAAGCGC 1201
Qy 1081 TGGAGAGAGAGAGGTTCTCCAGAGTCGGAAGTGA 1116
Db 1202 TGGAGAGAGAGAGGTTCTCCAGAGTCGGAAGTGA 1237

RESULT 9

US-09-925-301-207
; Sequence 207, Application US/09925301
; Patent No. US2002005308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925.301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 207
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-301-207

Query Match 100.0%; Score 1115.6; DB 9; Length 1996;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1115; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCTGCAACCTGTGAGATTAGCAACATTTTATAGCACTACTTCACTGCGATGTACAC 60
DB 141 ATGGCTGCAACCTGTGAGATTAGCAACATTTTATAGCACTACTTCACTGCGATGTACAC 200
QY 61 TCGGAGACCTCCACCTGCGCTCTGTTCCCTGCTGCGACCTTTGGGGCCGAGTACTTG 120
DB 201 TCGGAGACCTCCACCTGCGCTCTGTTCCCTGCTGCGACCTTTGGGGCCGAGTACTTG 260
QY 121 GTAACGACCTGAGCAACCCCGAGATGTATTGGAGGGTACAGAGAGCCAGCTGGTTG 180
DB 261 GTAACGACCTGAGCAACCCCGAGATGTATTGGAGGGTACAGAGAGCCAGCTGGTTG 320
QY 181 GGGGAAACAGCCCGCTTCTGCTGAGAGCGAGGTTCTGATCTGATCTGATCTGATCTG 240
DB 321 GGGGAAACAGCCCGCTTCTGCTGAGAGCGAGGTTCTGATCTGATCTGATCTGATCTG 380
QY 241 GAGAGAAACAGTACGAGCGAGCGCAATTCCTTCAAGAGCCCTTACGCCAGATGGGCC 300
DB 381 GAGAGAAACAGTACGAGCGAGCGCAATTCCTTCAAGAGCCCTTACGCCAGATGGGCC 440
QY 301 ACCCTGCAATTGTGCTTGTGAGAGCTGCTGCTGCTTGTGGGCTTGGGGGACCA 360
DB 441 ACCCTGCAATTGTGCTTGTGAGAGCTGCTGCTGCTTGTGGGCTTGGGGGACCA 500
QY 361 CTCATGCTGAGCTGCGAGACCTTCACTTCCAGCTCTTCTGATGAGCTCACTGATGAT 420
DB 501 CTCATGCTGAGCTGCGAGACCTTCACTTCCAGCTCTTCTGATGAGCTCACTGATGAT 560
QY 421 GAGCTGTGAGAGAGATGGCATGGCTTCTTCAAGAGCCCTTACGCCAGATGGGCC 480
DB 561 GAGCTGTGAGAGAGATGGCATGGCTTCTTCAAGAGCCCTTACGCCAGATGGGCC 620
QY 481 CAGGGACAGCCCTTGTGCGAGAGCTCTGAGACAGCTGACAGAGCCAGCCCTTAC 540
DB 621 CAGGGACAGCCCTTGTGCGAGAGCTCTGAGACAGCTGAGAGCCAGCCCTTAC 680
QY 541 CCGGGACGCTGTGCGAGAGAGCCCTTCTGCGAGCTTGTGAGCTTCTTCCACCGCAG 600
DB 681 CCGGGACGCTGTGCGAGAGAGCCCTTCTGCGAGCTTGTGAGCTTCTTCCACCGCAG 740
QY 601 ACTGCTGCTTCTGCGAGCTCTTCACTTCTTCAAGCTCTGAGAGCTGAGAGCTGAG 660
DB 741 ACTGCTGCTTCTGCGAGCTCTTCACTTCTTCAAGCTCTGAGAGCTGAGAGCTGAG 800
QY 661 CCCACTGATGGCAAGCTCTTCCCGAGGATGTTTCTGTACTGCAAGAGGGGATCCC 720
DB 801 CCCACTGATGGCAAGCTCTTCCCGAGGATGTTTCTGTACTGCAAGAGGGGATCCC 860
QY 721 AAGCAGCGGAAACGGAACGAGCGCCGCGGAAAGCTGAGCAAGAGTCTGGACTGT 780
DB 861 AAGCAGCGGAAACGGAACGAGCGCCGCGGAAAGCTGAGCAAGAGTCTGGACTGT 920
QY 781 CTGAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 921 CTGAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
QY 841 GACATCTCTCAACCGGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 981 GACATCTCTCAACCGGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040
QY 901 GAGCTCTTCAAGTCTGCGCTCGAGAGCTGAGCCCACTATGAGGGCCAAAGAGAGAG 960
DB 1041 GAGCTCTTCAAGTCTGCGCTCGAGAGCTGAGCCCACTATGAGGGCCAAAGAGAGAG 1100
QY 961 AACGAGCAATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 1101 AACGAGCAATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1160
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RESULT 10

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US-10-264-049-756
; Sequence 756, Application US/10264049
; Publication No. US2004000579A1
; GENERAL INFORMATION:
; APPLICANT: Bire et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FIVE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 756
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-049-756
```

Query Match 99.9%; Score 1114.4; DB 16; Length 1956;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1112; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCTGCAACCTGTGAGATTAGCAACATTTTATAGCACTACTTCACTGCGATGTACAC 60
DB 161 ATGGCTGCAACCTGTGAGATTAGCAACATTTTATAGCACTACTTCACTGCGATGTACAC 220
QY 61 TCGGAGACCTCCACCTGCGCTCTGTTCCCTGCTGCGACCTTTGGGGCCGAGTACTTG 120
DB 221 TCGGAGACCTCCACCTGCGCTCTGTTCCCTGCTGCGACCTTTGGGGCCGAGTACTTG 280
QY 121 GTAACGACCTGAGCAACCCCGAGATGTATTGGAGGGTACAGAGAGCCAGCTGGTTG 180
DB 281 GTAACGACCTGAGCAACCCCGAGATGTATTGGAGGGTACAGAGAGCCAGCTGGTTG 340
QY 181 GGGGAAACAGCCCGCTTGTGCTGAGAGCGAGGTTCTGAGCTGATCACTACCAAGTG 240
DB 341 GGGGAAACAGCCCGCTTGTGCTGAGAGCGAGGTTCTGAGCTGATCACTACCAAGTG 400
QY 241 GAGAGAAACAGTACGAGCGAGCGCAATTCCTTCAAGAGCTGAGAGAGAGAGAGAGAG 300
DB 401 GAGAGAAACAGTACGAGCGAGCGCAATTCCTTCAAGAGCTGAGAGAGAGAGAGAGAG 460
QY 301 ACCCTGCAATTGTGCTTGTGAGAGCTGCTGCTGCTTGTGGGCTTGGGGGACCA 360
DB 461 ACCCTGCAATTGTGCTTGTGAGAGCTGCTGCTGCTTGTGGGCTTGGGGGACCA 520
QY 461 ACCCTGCAATTGTGCTTGTGAGAGCTGCTGCTGCTTGTGGGCTTGGGGGACCA 520
DB 521 CTCATGCTGAGAGAGATGGCATGGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 580
QY 521 CTCATGCTGAGAGAGATGGCATGGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 580
QY 421 GAGCTGTGAGAGAGATGGCATGGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 581 GAGCTGTGAGAGAGATGGCATGGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 640
QY 481 CAGGGACAGCCCTTGTGCGAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 641 CAGGGACAGCCCTTGTGCGAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
QY 541 CCGGGACGCTGTGCGAGAGAGCCCTTCTGCGAGCTTGTGAGCTTCTTCCACCGCAG 600
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Db 701 CCCGCGAGCTGTGGCGGAGAGCCCCCTCCCGYGGCAGCTCTGACGTCCTCCACCGCAGGG 760
Qy 601 ACTGTGCTCTCTGGAGCTCCCACTCTCAGACTCCGGTGGAAATGACCTGTGACCTTGGAT 660
Db 761 ACTGTGCTCTCTGGAGCTCCCACTCTCAGACTCCGGTGGAAATGACCTGTGACCTTGGAT 820
Qy 661 CCCACTGATGGCAAGCTCTCCCGAGGATGTGTTTGTGACCTGCAAGAGGGGGATCCC 720
Db 821 CCCACTGATGGCAAGCTCTCCCGAGGATGTGTTTGTGACCTGCAAGAGGGGGATCCC 880
Qy 721 AACGCGGGAAGCGGAAACGAGCGCGCCCGAAAGCTGACCAAGAGTACTGGAATGT 780
Db 881 AACGCGGGAAGCGGAAACGAGCGCGCCCGAAAGCTGACCAAGAGTACTGGAATGT 940
Qy 781 CTGAGGGGCAAGAGAGCAAGCAAGCGCCCAAGAGGACCCACTGTGTGGAGTTCTATCCG 840
Db 941 CTGAGGGGCAAGAGAGCAAGCAAGCGCCCAAGAGGACCCACTGTGTGGAGTTCTATCCG 1000
Qy 841 GACATCTCTCACTCCAGCCCGAGCTCAACGAGGGGCTCTATGAAAGTGGAGAAATCCGATGAA 900
Db 1001 GACATCTCTCACTCCAGCCCGAGCTCAACGAGGGGCTCTATGAAAGTGGAGAAATCCGATGAA 1060
Qy 901 GGGGCTTCAAGTCTCTGCGCTCGAGGCTGTGGCCCACTATGTGGGCCCAAAAGAAAAG 960
Db 1061 GGGGCTTCAAGTCTCTGCGCTCGAGGCTGTGGCCCACTATGTGGGCCCAAAAGAAAAG 1120
Qy 961 AACGCACTGACCTACCTACGAGAGCTGAGCGCGCCCTGAGGTTCTACTCAAAACGGGAG 1020
Db 1121 AACGCACTGACCTACCTACGAGAGCTGAGCGCGCCCTGAGGTTCTACTCAAAACGGGAG 1180
Qy 1021 ATCTGGAAGGGGTGATGAGCGCGCGCACTGTCTCAAGTTTGGCAAAACTCAAGCGGC 1080
Db 1181 ATCTGGAAGGGGTGATGAGCGCGCGCACTGTCTCAAGTTTGGCAAAACTCAAGCGGC 1240
Qy 1081 TGAAGGAGGAGAGGTTCTCAAGTCTGAGTCTGAACTGA 1116
Db 1241 TGAAGGAGGAGAGGTTCTCAAGTCTGAGTCTGAACTGA 1276

RESULT 11
US-10-131-410-64
; Sequence 64, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-410-64

Query Match 83.6%; Score 933; DB 15; Length 2269;
Best Local Similarity 99.3%; Pred. No. 7.5e-265;
Matches 958; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
Qy 152 TGAAGGTAAGAGAGCCAGCTGTTGGGGGAACAGCCCAAGTTCTGTGCAAGACGC 211

Db 4 TGGCCCTTGAGAGAGGCGACAGCTGTGGGGGAACAGCCCAAGTTCTGTGCAAGA-GC 62
Qy 212 AGGTTTGAAGTGTGATCACTACCAAGTGAAGAAAGAAAGTACAGACGCAAGGCCATTG 271
Db 63 AGGTTTGAAGTGTGATCACTACCAAGTGAAGAAAGAAAGTACAGACGCAAGGCCATTG 122
Qy 272 ACTTCTCAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 331
Db 123 ACTTCTCAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 182
Qy 332 GTCTGTCTTTTGGGCTCTGGGGGCAAACTTCATGCTCCAGCTGCGAGACTTCACTTCCA 391
Db 183 GTCTGTCTTTTGGGCTCTGGGGGCAAACTTCATGCTCCAGCTGCGAGACTTCACTTCCA 242
Qy 392 GCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 451
Db 243 GCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 302
Qy 452 AGGAGGCCCTAGACCCAGGGGCTTTGACACAGGGGAGCCCTTTGGCCAGAGCTGTGG 511
Db 303 AGGAGGCCCTAGACCCAGGGGCTTTGACACAGGGGAGCCCTTTGGCCAGAGCTGTGG 362
Qy 512 ACAGCGGTGAGCAAGCCAGCCCTTACCAACCCCGGAGCTGTGGCGCAGAGAGCCCTCC 571
Db 363 ACAGCGGTGAGCAAGCCAGCCCTTACCAACCCCGGAGCTGTGGCGCAGAGAGCCCTCC 422
Qy 572 CTGGCAGCTCTGACCTCTCACCGCA-GGACTGTGCTCTGAGACTCTTCTGAGACTCTTCA 631
Db 423 CTGGCAGCTCTGACCTCTCACCGCA-GGACTGTGCTCTGAGACTCTTCTGAGACTCTTCA 481
Qy 632 ACTCGGTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 691
Db 482 ACTCGGTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 541
Qy 692 GTTTTGTGATCTGCAAGAGGGGGATCCCAAGCAGCGGAAACGAGCGCGGCC 751
Db 542 GTTTTGTGATCTGCAAGAGGGGGATCCCAAGCAGCGGAAACGAGCGCGGCC 601
Qy 752 GAAAGCTGAGCAAGAGTCTGGAAGTGTCTGAGGGCAAGAGAGCAAGACAGCGGCCCA 811
Db 602 GAAAGCTGAGCAAGAGTCTGGAAGTGTCTGAGGGCAAGAGAGCAAGACAGCGGCCCA 661
Qy 812 GAGGCAACCACTGTGGAGTTCATCCGGGACATCTCTCAACCCGGAGCTCAAGAG 871
Db 662 GAGGCAACCACTGTGGAGTTCATCCGGGACATCTCTCAACCCGGAGCTCAAGAG 721
Qy 872 GCCTCATGAAGTGGAGATTCGGCATGAAGGCGTCTTCAAGTTCTCGCGCTCGAGGCTG 931
Db 722 GCCTCATGAAGTGGAGATTCGGCATGAAGGCGTCTTCAAGTTCTCGCGCTCGAGGCTG 781
Qy 932 TGGCCCACTATGTGGGCGCAAAAGAAAGACAGCACTGACTGAGAGCTGAGCC 991
Db 782 TGGCCCACTATGTGGGCGCAAAAGAAAGACAGCACTGACTGAGAGCTGAGCC 841
Qy 992 GGGCCATGAGATCTACTCAACCGGAGATCTTGAAGGGGTGATGAGCGCGGACTG 1051
Db 842 GGGCCATGAGATCTACTCAACCGGAGATCTTGAAGGGGTGATGAGCGCGGACTG 901
Qy 1052 TCTACAGTTTGGCAAAACTCAAGCGGCTGAGAGAGAGAGGTTCTCAAGTCTGCA 1111
Db 902 TCTACAGTTTGGCAAAACTCAAGCGGCTGAGAGAGAGAGGTTCTCAAGTCTGCA 961
Qy 1112 ACTGA 1116
Db 962 ACTGA 966

RESULT 12
US-09-922-217-853/c
; Sequence 853, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:

```
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Wang, Yugu
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471C13
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 853
LENGTH: 626
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-217-853
```

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Query Match      55.9%; Score 624.4; DB 9; Length 626;
Best Local Similarity 99.8%; Pred. No. 7e-174;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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155 AGGGTACAGAGAGAGCCAGCTGGTTGGGGAGACGCCCACTTGTGTGAGAACGACAG 214
626 AGGGTACAGAGAGAGCCAGCTGGTTGGGGAGACGCCCACTTGTGTGAGAACGACAG 567
215 TTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 274
566 TTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 507
275 TCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 334
506 TCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447
335 TGGTCTTTGGGCTCTGGGGAGACCACTGATGATGATGATGATGATGATGATGAT 394
446 TGGTCTTTGGGCTCTGGGGAGACCACTGATGATGATGATGATGATGATGATGAT 387
395 CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 454
386 CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327
455 AGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 514
326 AGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267
515 AGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 574
266 AGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
575 GAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCT 634
206 GAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCT 147
635 CCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 694
146 CCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 87
695 TTCTGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 754
86 TTCTGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 27
755 AGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
26 AGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1
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RESULT 13
US-09-833-263-853/c
Sequence 853, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 853
LENGTH: 626
TYPE: DNA
ORGANISM: Homo sapien
US-09-833-263-853
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Query Match      55.9%; Score 624.4; DB 9; Length 626;
Best Local Similarity 99.8%; Pred. No. 7e-174;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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155 AGGGTACAGAGAGAGCCAGCTGGTTGGGGAGACGCCCACTTGTGTGAGAACGACAG 214
626 AGGGTACAGAGAGAGCCAGCTGGTTGGGGAGACGCCCACTTGTGTGAGAACGACAG 567
215 TTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 274
566 TTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 507
275 TCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 334
506 TCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447
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446 TGGTCTTTGGGCTCTGGGGAGACCACTGATGATGATGATGATGATGATGATGAT 387
395 CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 454
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326 AGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267
515 AGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 574
266 AGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
575 GAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCT 634
206 GAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCT 147
635 CCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 694
146 CCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 87
695 TTCTGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 754
86 TTCTGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 27
755 AGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
26 AGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1
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RESULT 14

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US-10-025-380-853/c
; Sequence 853, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secretist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 853
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-853

Query Match      55.9%; Score 624.4; DB 13; Length 626;
Best Local Similarity 99.8%; Pred. No. 7e-174;
Matches 625; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Query      695 TTCGTGACCTGCAAGAGAGGGGATCCCAAGCAGCGGAAAGCGGAGCCCGCGAA 754
Db          86 TTCGTGACCTGCAAGAGAGGGGATCCCAAGCAGCGGAAAGCGGAGCCCGCGAA 27

Query      755 AGCTGAGCAAGAGTACTGGAGCTGT 780
Db          26 AGCTGAGCAAGAGTACTGGAGCTGT 1

RESULT 15
US-09-922-217-944/c
; Sequence 944, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secretist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 944
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-944

Query Match      50.3%; Score 561.4; DB 9; Length 563;
Best Local Similarity 99.8%; Pred. No. 2.7e-155;
Matches 562; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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